

STIC Database Tracking Number: 9427

TO: Manjunath N Rao

Location: CM1/10D01/10A11

Art Unit: 1652

Wednesday, May 28, 2003

Case Serial Number: 040863

From: Susan Hanley

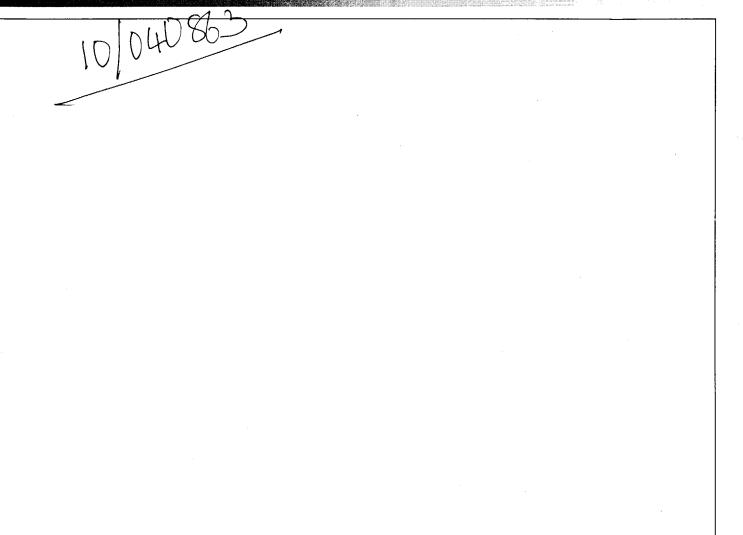
Location: Biotech-Chem Library

CM1-6B05

Phone: 305-4053

susan.hanley@uspto.gov

Search Notes





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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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using sw model OM protein - protein search,

May 27, 2003, 15:01:52 ; Search time 37.6369 Seconds (without alignments) 1932.533 Million cell updates/sec Run on:

US-10-040-863-10

1 LQQRIVKLQPLSEKELPMTT......RSHFHLKAKGVTCYVAGRAF 353 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 6.5 Scoring table:

671580 Total number of hits satisfying chosen parameters:

671580 seqs, 206047115 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp_archea:* sp_bacteria:* SPTREMBL_21:* Database

sp_vertebrate:*
sp_unclassified:* sp_invertebrate:* sp_organelle:*
sp_phage:*
sp_plant:* sp_rvirus:*
sp_bacteriap:* sp_archeap: sp_rodent:* sp_virus:* sp_mammal:* sp_fungi:* sp_human:* sp_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

cercc hylob mus ratt mus	Q14338 homo sapien Q920t4 mus musculu Q91v73 mus musculu Q94515 macaza faso	callithri macaca mu bos tauru macaca fa		gorii eulem hylok macac pongo	mace homc pan homc
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ALIGNMENTS

353 PRT; PRELIMINARY; 055025 RESULT I

01-JUN-1998 (TrEMBLrei. 06, Created)
01-JUN-1998 (TrEMBLrei. 06, Last sequence update)
01-MR-2002 (TrEMBLrei. 20, Last annotation update)
Alpha 1,2 fucosyltransferase (Fragment).
Rattus norvegicus (Rat)
Buxaryota, Medrazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia; Butheria: Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

SEQUENCE FROM N.A. STRAIN-BUFFALO RAT;

MEDITINE 98342056; PubMed=9675030; Sherwood A.L., Holmes E.H.; Sherwood A.L., Holmes E.H.; "Cloning and expression of the catalytic domain from rat hepatoma H35 cell GDP-fucose: GMI alpha 1->Ziucosyltransferase, an enzyme which is activated during early stages of chemical carcinogenesis in rat Arch. Biochem. Blophys. 355:215-221(1998).
EMBL; AF042743; AAC14695.1;
InterPro: IPR002516; Gr_ll.
Pfam. PF01531; Glyco_transf_ll; 1.
Glycosyltransferase; Transferase.
NON_TER liver.

Gaps 0; 100.0%; score 1896; DB 11; Length 353; 100.0%; Pred. No. 4.3e-164; ive 0; Mismatches 0; Indels 0; Local Similarity 100. mes 353; Conservative Query Match Matches

353 AA; 39738 MW; 609D64EB222C9585 CRC64;

SEQUENCE

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1 LOORIVKLOPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNOM 60 1 LQORIVKLQPLSEKELPMITQMSSGNIESPEMRRDSBQHGNGELÄGMFINSIGRLGNQM 60 Dp δy

61 GEYATLFALARMNGRLAFIPASMENALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120 QΫ́

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RESULT 4
         RESULT 3
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GEYATLFALARMNGRLAFIPASMENALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120
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                      YRIIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREBAQAFLRGLRVNGSQPSTFV
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"An amino acid region at the N-terminus of rat hepatoma H35 cell
fucose:GM1 alpha 1-2 fucosyltransferase is required for optimum
activity and interaction with lipids.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF264005; AAF72200.1;
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SEQUENCE 380 AA; 42742 MW; 920692C96689C05C CRC64;
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Last annotation update)
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Pred. No. 4.7e-164;
0; Mismatches 0;
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Pfam; PF01531; Glyco_transf_11; 1.
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100.0%;
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
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Best Local Similarity
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Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
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Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB006138; BAA21742.1;
Interpro; IPR002516; GT_11.
Pfam; PF01531; GJyco_transf_11; 1.
Glyco_transferase; Transferase.
SEQUENCE 354 AA; 39995 MW; 8636444888215BA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                 Soejima M., Wang B., Koda Y., Kimura H.;
"Two distinct rat GDP-L-fucose:b-D-galactoside 2-a-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
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                                            01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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100.0%; Pred. No. 1.5e-150;
tive 0; Mismatches 0;
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Alpha 1,2-fucosyltransferase B.
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Mammalia; Eutheria;
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Query Match
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"Molecular Cloning, Genomic Mapping, and Expression of Two Secretor Blood Group alpha (1,2)Fucosyltransferase Genes Differentially Regulated in Mouse Uterine Epithelium and Gastrointestinal Tract.";
J. Biol. Chem. 276:23748-23756(2001).
BMBL; AF214656; AAF45146.1;
MGD; MGI:109374; Fut2.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
               Liehr T., Le Pendu J.;
"Comparison of the three rat GDP-L-fucose: beta-D-galactoside 2-alpha-L-fucosyltransferases FTA, FTB and FTC.";
Eur. J. Blochem. 268:106-1019(2001).
EMBL, AF131238; AAD24469.1;
InterPro; IPR002516; GT_11.
FTAN FF01531; GIyco_transf_11; 1.
Glycosyltransferase; Transferase.
SEQUENCE 354 AA; 39983 MW; 123E8C8379E8559E CRC64;
Bureau V., Marionneau S., Cailleau-Thomas A., Le Moullac-Vaidye Liehr T., Le Pendu J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11; Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                    ó
                                                                                                                                            Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17; Indels
                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Glycosyltransferase; Transferase.
SEQUENCE 347 AA; 39243 MW; DD5F441046CC8E79 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (TrEMBLrel. 15, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Alpha(1,2)fucosyltransferase FUT2 (EC 2.4.1.69).
                                                                                                                                           92.1%; Score 1747; DB 11;
100.0%; Pred. No. 1.5e-150;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.1%; Score 1538.5; DB 11
89.0%; Pred. No. 1.4e-131;
tive 12; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            347 AA
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01-0CT-2000 (TrEMBLrel. 15, Last sequ
01-MAR-2002 (TrEMBLrel. 20, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKVFKPEAAFLPEWVGIPADLSPLLK 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               328 LKVFKPEAAFLPEWVGIPADLSPLLK 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=129/OLA;
MEDLINE=21316545; PubMed=11323419;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 89.0
nes 290; Conservative
                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Mouse).
                                                                                                                                              Query Match
Best Local Similarity
Matches 326; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
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Matches
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Q9JL27
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YRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQARURGLRVNGSQPSTFV 180
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                                                                                                                                                                                                                                                                                                                                                                                                                  260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIXLANYTLPDSPF 300
                                                                                                             61 GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLUDWMEER 120
                                                                                                                                               180
                                                                                                                                                                                                                                                                                        141 YRHIPGGYVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFV 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261 LGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLFDSPF 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM 60
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09
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                                                                                                                                                                                                                                                                                                                                                             GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
LQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM
                                           EC EC
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01-AGG-1998 (TrEMBLrel. 07, Last sequence update)
01-AGR-2002 (TrEMBLrel. 20, Last annotation update)
01-AGR-2002 (TrEMBLrel. 20, Last annotation update)
6DP-L-fucoses:beta-D-galactoside 2-alpha-1-fucosyltransferase
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88.7%; Pred. No. 3.1e-131;
Live 13; Mismatches 17; Indels
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Glycosyltransferase; Transferase.
SEQUENCE 347 AA; 39215 MW; 616CCB11581C4179 CRC64;
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STRAIN-ICR; TISSUE-GASTROINTESTINAL TRACT;
MEDLINE-20471982; Pubmed-11018479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochim. Biophys. Acta 1487:275-285(2000).
EMBL; AF064792; AAC16887.1;
MGD; MGI:109374; Fut2.
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PRELIMINARY;
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                       291VF0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YRHIPGQYVRFTGYPCSWTFYHHLRPEILKEFILHDHVREEAQAFLRGLRVNGSQPSTFV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247 LGDVVFAGNGIEGSPAKDFALLTQCNHTIMITIGTFGIWAAYLAGGDTIYLANYTLPDSPF 306
                          201 GVHVRRGDYVHVMPKVWKGVVADRGYLEKALDRFRARYSSPVFVVTSNGMAWCRENINTS 260
                                                                                                                YRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFV 180
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GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus spicilegus (Steppe mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.2%; Score 1483.5; DB 11; Length 321; 88.9%; Pred. No. 1.2e-126; Live 11; Mismatches 17; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DBC-2002 (TrEMBLrel. 21, Last annotation update)
GDP-Urlucose:beta-D-galactoside 2-alpha-1-fucosyltransferase
FUT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Five Mus musculus subspecies.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB039123; BAB68647.1;
InterPro: IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Glycosyltransferase; Transferase.
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36560 MW; 5B7D19BA6D4B5394 CRC64;
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                                                                                                                                                                                                                                                                                                                                              PRT;
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LKIFKPAAFLPEWM 321
                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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321 AA;
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SEQUENCE
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Q91VF0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIRALING STRAINS:
Liu Y., Kitano T., Kolde T., Shiroishi T., Moriwaki K., Saitou N.;
Liu Y., Kitano T., Kolde T., Shiroishi T., Moriwaki K., Saitou N.;
"Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 LQQRIVKLQTLSEKEL-QAVQMSSPNAARTDMQQ-----SAKLQGIFTINSIGRLGNQM
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 21, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase (EC 2.4.1.69) (Fragment).
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLPel. 21, Last annotation update)
(ECP-L-fucose:bbeta-D-galactoside 2-alpha-1-fucosyltransferase
(EC 2.4.1.69) (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Five Mus musculus subspecies.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB039114; BAB68638.1; -.
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36516 MW; 0622D3BB503B72D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.2%; Score 1483.5; DB 11;
88.6%; Pred. No. 1.2e-126;
ive 12; Mismatches 17; Ir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Glycosyltransferase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AB039115, BAB68639.1, EMBL, AB039116, BAB68640.1, EMBL, AB039117, BAB68641.1, EMBL, AB039118, BAB68642.1, EMBL, AB039119, BAB68643.1, EMBL, AB039120, BAB68644.1, EMBL, AB039120, BAB68684.1, EM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 LKVFKPEAAFLPEWV 315
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LKIFKPAAFLPEWM 321
                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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3

us-10-040-863-10.rspt

musculus (Mouse).

SEQUENCE Query Match

29

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Gaps

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257 HGDVVFAGDGIEGSPAKDFALLTQCNHTIMITIGTFGIWAAYLTGGDTIXLANYTLPDSPF 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF 300
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                                                                                                                                                                                                                                                        1 LQQRIVKLQPLSEKELPWTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM
                                                                                                                                                                                                                                                                                                     28 VQQRLAKIQAM--WELPV-----OIPVLASTSKALGPSOLRGMWFINAIGRLGNQM
                                                                                                                                                                                                                                                                                                                                                  GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197 GVHVRRGDYVHVMPKVWKGVVADRRÝLQQALDWFRARYSSPIFVVTSNGMAWCRENIDIS
                                                                                                                                                                                                                                                                                                                                                                                                                                        121 YRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.7%; Score 1397.5; DB 6; Length 338; 79.4%; Pred. No. 8.7e-119; Live 27; Mismatches 29; Indels 11;
                                                                                                                                                             DB 6; Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apoil P.-A., Roubinet F., Despiau S., Mollicone R., Oriol R.,
                                                                                                                                                                                                             Indels
J. Biol. Chem. 270:4640-4649(1995).

EMBL; AB015635, BAA31128.1; -.

InterPro; IPR002516; GT_11.

Pfam; PF01531; Glyco_transf_11; 1.

Glycosylten:Fersas, Transferase.

SEQUENCE 343 AA; 38973 MW; 894E28BD74AEBFBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        338 AA; 38428 MW; E7FABAOFF1BC95F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Alpha (1,2) fucosyl transferase.
                                                                                                                                                             Query Match 73.9%; Score 1400.5; DB 6; Best Local Similarity 79.8%; Pred. No. 4.8e-119; Matches 260; Conservative 25; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 338 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 LKVFKPEAAFLPEWVGIPADLSPLLK 326
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EMBL; AF080604; AAF14066.1; -
InterPro: IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
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MEDLINE=20188794; PubMed=10723735;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Simi
Matches 259;
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SEQUENCE
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Koda Y., Tachida H., Soejima M., Takenaka O., Kimura H.;
"The old origin of a null allele se428 of the human ABO-secretor type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEYATLFALARMNGRIAFIPESMHNALAPIFRISLPVLHSDTARRIPWQNYHLNDWMEER 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120
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MEDILINE=9181460; Pubmed=7876235;
Kelly R.J., Rouquier S., Giorgi D., Lennon G.G., Lowe J.B.;
"Sequence and expression of a candidate for the human secretor blood group alpha(1,2) fucosyltansferase gene (FUT2).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM 60
                                                                                                                                                                                     Genes
                                                                                                                                                               Saitou N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 LQQQIVKLQTLSEKEL-QAVQMSSPNAARTDMQQ-----SAKLQGIFTINSIGRLGNQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 GVHVRRGDXVHVMPKVWKGVVADRGYLERALDRERARYSSPVFVVTSNGMAMCRENINTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 LGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF
                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotā; Metazoā; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11; Length 321;
                                                                                                                                STRAIN=NJL/MSF;
Liu Y., Kitano T., Koide T., Shiroishi T., Moriwaki K., Saitou
"Conspicuous Differences among Gene Genealogies of 21 Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alpha(1,2) fucosyltransferase gene (FUT2).";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                   Five Mus musculus subspecies.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AB039122; BAB6866.1; -.
InterPro; IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Glycosyltransferase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                        321 AA; 36464 MW; FF5304CD150F774A CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
                                                                                                                                                                                                                                                                                                                                                                                                                                   77.5%; Score 1468.5; DB L
87.9%; Pred. No. 2.8e-125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13; Mismatches
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01-NOY-1998 (TEMBLEL: 08, Le
01-NOY-1998 (TEMBLEL: 20, Le
Alpha(1,2) fucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gorilla gorilla (gorilla).
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Matches 277; Conservative
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                                                                                                                                                                                                                                                                                                                                                                   321
                                                                                                                SEQUENCE FROM N.A.
                                                                  NCBI_TaxID=10090;
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077486

RESULT 10 077486 ē

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Kelly R.J., Rouquier S., Giorgi D., Lennon G.G., Lowe J.B.;
"Sequence and expression of a candidate for the human secretor blood group alpha(1,2) fucosyltansferase gene (FUT2).";
J. Biol. Chem. 270:4640-4649(1995).
EMBL: AB015634: BAA31127.1:
Interpro: IPR002516: GT_11.
Fign: PF01531: Glyco_transf_11; 1.
Glycosyltransferase: Transf_li 1.
Glycosyltransferase: Transf_erase.
SEQUENCE 343 AA; 38999 MW; B849D7E152852081 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 VQQRLAKIQAM--WELPV-----QIPVLASTSKALGPSQLRGMWTINAIGRLGNQM 76
GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER
                241 RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF
                                                                                                                                                                          252 HGDVVFAGDGIEGSPAKDFALLIQCNHTIMIGTFGIWAAYLIGGDIIYLANYTLPDSPF
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                                                   121 YRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFV
                                                                                                      181 GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS
                                                                                                                                                                                                                                                                                                                                                                                             Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Pan.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                        AA.
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01-NOV-1998 (TEBMBLrel. 08, Cre
01-NOV-1998 (TEBMBLrel. 08, Las
01-MAR-2002 (TEBMBLrel. 20, Las
Alpha(1,2)fucosyltransferase.
FUI2.
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257 HGDVVPAGDGIBGSPAKDFALLTQCNHTIMTIGTFGIWAAYLJGGDTIYLANYILFDSPF 316
RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apoll P.-A., Roubinet F., Despiau S., Mollicone R., Oriol R., Blancher A.;
"Evolution of alpha2-Fucosyltransferase genes in primates: relation between an intronic Alu-Y element and red cell expression of ABH mol. Biol. Evol. 17:337-351(2000).
EMBL; AF080606; AAF14068-1;
DiterPro; IPR002216; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LOORIVKLOPLSEKELPMTTOMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNOM
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 343;
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Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-MAR-2002 (TrEMBLrel. 20, Last anno
Alpha (1,2) fucosyl transferase.
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MEDLINE=20188794; Pubmed=10723735;
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Best Local Similarity
Matches 259; Conserv
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Q29505;
01-FEB-1997 (
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Hitoshi S., Kojima N., Kanazawa I., Tsuji S.;
"Modicular cloning and expression of a third type of rabbit GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase.";
J. Biol. Chem. 271:16975-1169161961).
--- FUNCTION: CREATES A MEMBRANE-ASSOCIATED PRECURSOR OLIGOSACCHARIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Galactoside 2-L-fucosyltransferase 3 (EC 2.4.1.69) (Secretor blood
group ALPHA-2-fucosyltransferase) (GDP-L-fucose:beta-D-galactoside
2-ALPHA-L-fucosyltransferase) (ALPHA(1,2)FT) (Fucosyltransferase 3
Oryctolagus cuniculus (Rabbit).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Eutelecstomi;
Mammalia: Butheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
LUMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                    EXPRESSED IN A TISSUE-SPECIFIC MANNER.
SIMILARITY: STRUCTURAL SIMILARITY WITH THE OTHER MAMMALIAN GLYCOSYLIRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002516; GT 11.
Pfam; PF01531; Glyco_transf_11; 1.
Iransferase; Glycosyltransferase; Glycoprotein; Iransmembrane; Signal-anchor; Golgi stack.
                                                                                                               [1]
SEQUENCE FROM N.A.
TISSUE-GASTROINTESTINAL TRACT;
MEDLINE-962792911; PubMed-8663168;
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286 N
312 N
39469 MW;
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192
286
312
347 AA;
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Gaps
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                                   73.4%; Score 1391.5; DB 6; Length 347; 79.8%; Pred. No. 3.2e-118; tive 25; Mismatches 34; Indels 7;
746F7007309862A5 CRC64;
                              Query Match
Best Local Similarity 79.84
Matches 260; Conservative
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1;

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GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120
LQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM 60
                           LOQRLVRIOPTWEELLPAL-----TPAVTFRPTSORAPSRPLGGMWTINAMGRLGNQM 80
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YRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFV 180 121

GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS

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RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF 201

LKVFKPEAAFLPEWVGIPADLSPLLK 326

321

192 301

Koda Y., Tachida H., Soejima M., Takenaka O., Kimura H.; "The old origin of a null allele se428 of the human ABO-secretor type alpha(1,2) fucosyltransferase gene (FUT2)."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases. HENDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTEGIWAAYLAGGDTIYLANYTLPDSPF 316 MEDLINE-95181460; PubMed=7876235; Relly R.J., Rouquier S., Glorgi D., Lennon G.G., Lowe J.B.; Relly R.J., Rouquier S., Glorgi D., Lennon G.G., Lowe J.B.; Relly R.J., Rouquier S., Glorgi D., Lennon G.G., Lowe J.B.; Sequence and expression of a candidate for the human secretor blood group alpha(1,2) fucosyltansferase gene (FUT2)."; J. Fucosyltansferase gene (FUT2)."; J. Fusil. Chem. 270:4640-4649(1995).

InterPro: IPR015516; GT_11:
Pram. PF01531; GT_21:
Pram. PF01531; GT_20_transfell; 1.

Glycosyltransferase; Transferase.
SEQUENCE 343 AA: 38973 MW: 2BD4D2A9704F4A0C CRC64; GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120 1 LQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM 60 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Pongo. GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF DB 6; Length 343; 73.3%; Score 1389.5; DB 6; Leust... 79.1%; Pred. No. 4.8e-118; 79.1%; Pred. no. 4.8e-118; 08, Last sequence update) 20, Last annotation update) 343 AA Created) PRT; LKVFKPEAAFLPEWVGIPADLSPLLK 326 Eukaryota, Metazoa, Chordata; Mammalia, Eutheria, Primates; Alpha(1,2) fucosyltransferase (TrEMBLrel. 08, (TrEMBLrel. 20, (TrEMBLrel. 08, Pongo pygmaeus (Orangutan) PRELIMINARY; Matches 258; Conservative Similarity SEQUENCE FROM N.A. NCBI_TaxID=9600; 01-NOV-1998 (01-NOV-1998 (01-MAR-2002 (Query Match Local 077487 077487 121 181 241 61 17 137 301 197 Best 077487 ACCOOR NAME OF THE PROPERTY OF Qγ qq δŏ QQ δ g QQ ōλ á á

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Gaps

180 196 240

> completed: May 27, 2003, 15:10:46 He : 38.6369 secs Search cor Job time

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GenCore version 5.1.5 Copyright (c) 1993 - 2003 Compugen Ltd.
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May 26, 2003, 10.20:56; Search time 3089 72 Seconds
U5-10-040-863-7
table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 subset of hits satisfying chosen parameters: 0bB seq length: 200000000 Cessing: Minimum Match 100% Listing first 45 summaries GenEmbl:* GenEmbl:* 1 gb_ba:* 1 gb_ba:* 5 gb_po:* 1 gb_pr:* 2 gb_pr:* 1 gb_pr:* 1 gb_pr:* 1 gb_pr:* 1 gb_pr:* 2 gb_pr:* 1 gb_pr:* 1 gb_pr:* 2 gb_pr:* 1 gb_pr:* 2 gb_pr:* 2 gb_pr:* 3 gb_pr:* 4 gb_or:* 5 gb_pr:* 5 gb_pr:* 6 gb_pr:* 1 gb_pr:* 1 gb_pr:* 1 gb_pr:* 1 gb_pr:* 2 gb_pr:* 2 gb_pr:* 3 gb_pr:* 4 gb_or:* 5 gb_pr:* 5 gb_pr:* 5 gb_pr:* 6 gb_pr:* 7 gb_pr:* 1 gb_pr:* 1 gb_pr:* 1 gb_pr:* 2 gb_pr:* 2 gb_pr:* 2 gb_pr:* 3 gb_pr:* 4 gb_pr:* 3 gb_pr:* 4 gb_pr:* 3 gb_pr:* 4 gb_pr:* 4 gb_pr:* 5 gb_pr:* 6 gb_pr:* 6 gb_pr:* 7 gb_pr:* 7 gb_pr:* 8 gb
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Pred. No. is the number of results predicted by chance to have \boldsymbol{a}

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3.	798.	φ.	96	10	3912	122 Mus mus
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Sciurognathi, Muridae, Murinae,
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1,2-fucosyltransferase B (FTB) gene,
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Comparison of the three rat GDP-L-fucose:beta-D-galactoside
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Bureau,V., Le Moullac-Vaidye,B., Liehr,T., Denis,M. and
Direct Submission
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Eur. J. Biochem. 268 (4), 1006-1019 (2001)<sup>2</sup>
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Rattus norvegicus
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/protein_id="aAF72200.1"
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/translation="WASAQVPESFPLAHFLIFVFVPSTIIHLQQRIVKLQPLSEKELP
MTQMSSGNTESPEMRRDSBQHGNGELRGMFTINSIGRLGNQGEYATLFALARMNGR
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fucosyltransferase modulates enzyme activity and interaction with libids: strong preference for glycosphingolipids containing terminal Galbetal-SGalMAc-structures
Biochemistry 40 (19), 5708-5719 (2001)
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                                                                                                                                                                    Hospital,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 1149; DB 10; Length 1149; 100.0%; Pred. No. 7.8e-297; cive 0; Mismatches 0; Indels 0;
                                                                                                                                                                    Northwest
                                                                                                                                                                                  USA
                                                                                                        2 (bases 1 to 1149)
Sherwood, A.L. and Holmes, E.H.
Direct Submission
Submitted (05-MAY-2000) Molecular Medicine,
                                                                                                                                                                                      Seattle, WA 98134,
                                                                                                                                                                                                                                                                                                hepatoma"
                                                                                                                                                                                                                                          /organism="Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                     /note="glycosyltransferase'
                                                                                                                                                                                                                                                      /strain="Fischer"
/db_xref="taxon:10116"
/cell_line="Reuber H35
1. .1143
                                                                                                                                                                                                 Location/Qualifiers
1. .1149
                                                                                                                                                                                    2203 Airport Way South,
                                                      Biochemistry 40 (19),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 1149; Conservative
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11341836
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                                   CCTAATGTGTGGAAGGGCGTGGTGGCTGACCGGGGTTACCTGGAAAAGGCCCTGGATATG 720
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    ASCCAGCCGAGTACTTTGTGGGTGTCCATGTGCGCCGAGGGGACTATGTGCATGTCATG 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (04-AUG-1997) Yoshiro Koda, Kurume University, School
Medicine, Department of Porensic Medicine; Asahimachi 67, Kurume
Fukuoka 830, Japan (E-mail:ykoda@med.kurume-u.ac.jp,
Tel:0942-31-7554, Fax:0942-31-7700)
                                                   1171 ACCCTTCCGGATCTCCCGTTCCTCAAAGTCTTTAAGCCAGGGCAGCCTTCCTAACCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGGTCCCACTTCCACCTCAAGGCAAAAGGAGTCACTTGTTACGTCGCAGGAAGAGCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCCGGGCACGCTATTCATCTCCAGTCTTCGTGGTTACAAGCAACGGTATGGCCTGGTGC
                                                                                                            CGGGAGAACATTAATGCTTCCCGAGGAGACGTGGTGTTCGCGGGCAATGGTATTGAGGGG
                                                                                                                                                                                                                                               1051 TCGCCAGCCAAGGACTTCGCGCTCACCCAGTGCAACCACCATCATGACTATTGGG
                                                                                                                                                                                                                                                                               ACCTTTGGGATTTGGGCTGCCTACCTGGCAGGTGGTGATACCATCTACTTAGCCAACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                     TCGCCAGCCAAGGACTTCGCGCTGCTCACCCAGTGCAACCACCACCATCATGACTATTGGG
                                                                                                                                                                                                                                                                                                                                            ACCCTTCCGGATTCTCCGTTCTTCAAAGTCTTTAAGCCAGAGGCAGCCTTCCTACCCGAA
                                                                                                                                                                                                                                                                                                                                                                                                       TGGGTGGGCATCCCTGCCGATCTGTCCCCACTCTTAAGGCATTAACACCAGCCTGTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus FTB mRNA for alpha 1,2-fucosyltransferase, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus colon cancer cell_line:RCN-9 cDNA to mRNA.
Rattus norvegicus
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Two distinct rat GDP-L-fucose:b-D-galactoside
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Rattus norvegicus"
/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /map="1q22-q31"
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1. .2984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AB006138.1 GI:2317265
FTB; alpha 1,2-fucosyltransferase.
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TITLE
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
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KEYWORDS
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                                                                                                                                                                                                              /product-"alpha 1,2-fucosyltransferase B"

'protein_id="AAD24469.1"

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LAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFYRFTG
                                                                                                                                                                                                                                                                                                         YPCSWIFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVH
VMPNVWRGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGN
                                                                                                                                                                                                                                                                                                                                       GIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPE
AAFLPEWVGIPADLSPLLKH"
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В
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                                                                                                                                                                                  /note="glycosyltransferase; alpha 2-fucosyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1133.8; DB 10; Length 1847;
Pred. No. 9.3e-293;
); Mismatches 2; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
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                                                                                                                               /product="alpha 1,2-fucosyltransferase
organism="Rattus norvegicus"
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                               'db_xref="taxon:10116"
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                                                           /map="lq22-q31"
<211. .>1275
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                                              /chromosome="1
                                                                                                                                                                                                  /codon_start=]
                                                                                                       <211. .>1275
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                                                                                                                                                                                                                                                                                                                                                                                                                 98.78;
99.78;
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<211. .>1275
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Radio-Oduola,B., Ali-osman,F.R., Allen,C.,

Rabarda,J., Benton,J., Binage, M.C., Are,Y.R., Ayele,M., Banks,T.,

Barbaria,J., Benton,J., Binage, M.C., Blankenburg, K., Bonnin,D.,

Bunay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,

Carron,T.R., Carter,M., Cavacos,S.R., Chacko,J.C., Caveron,T.R., Corle,M.C.,

Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,

Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,

Davis,C., Davis,C., Coyle,M.D., Dathorne,S.R., David,R.,

Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,

Douthwaite,M.J., Draper,H., Dugan-Rochas,S., Dunbin,K.J.,

Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,

Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P. Frantz,P.,

Garrell,J.H., Guevara,W., Garner,T., Garza,N., Garla,R., Hernandez,J.,

Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,

Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,

Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Loulseged,H.,

Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,

Lozado,M.D., Waptan,P., Martin,R., Marbaka,R., Martinez,E.,

Mabsehwari,M., Mapua,P., Martin,R., Martin,R., Markson, M., Morris,S.,

Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Morsen,M.,

Miner,G., Miner,Z., Milchell,T., Morbabat,K., Mank,G., Markson,N.,

Maner, M., Markson, R., Markson, N., Manyen,N., Manyen,N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hinear HTG 24-JUL-2002
*** SEQUENCING IN PROGRESS
                                              CGGGAGAACATTAATGCTTCCCGAGGAGGACGTGGTGTTCGCGGGCAATGGTATTGAGGGG 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sclurognathi, Muridae, Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris, Moser,M., Neal,D., Newtson,J., Newtson,M., Nayen,A., Nguyen,N., Nguyen,N., Nguyen,N., Nguyen,N., Nguyen,N., Nguyen,N., Nguyen,N., Nguyen,N., Nguyen,M., Okw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCCTTCCGGATTCTCCGTTCCTCAAAGTCTTTAAGCCAGAGGCAGCCTTCCTACCCGAA
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/translation="MASAQVPESFPLAHFLIFVFVTSTIIHLQQRIVKLQPLSEKELP
ITQMSSGNTESPEMRRDSDQHGNGELRGMFTINSIGRLGANGGEYRTHIPGHFYRFTG
YPCSWFPXHHALAPILKEFTLENHYRERQARINGSQPSTFYGYVYRRGDYNH
VMPNVWKGVVADRGYLEKFFTLENHYRERQARINGSGPSTFYGYVYRRGDYNH
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GIEGSPAKDFALLTQQNHTMINIGTFGIWAAYLAGGDTIYLANYTLPDSSPELKVFKPE
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/product="alpha 1,2-fucosyltransferase"
/protein_id="BBA21742.1"
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Worley, K.C.

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Submitted (16-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

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Submitted (14-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Jul 19, 2002 this sequence version replaced gi:20806241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 63 contigs. The true order of the pieces is not known and their order in this sequence record is
Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Sooth, T., Shochtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Sutton, A., Tayor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, N., Tang, M., Usnasey, J., Tayor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Wang, S., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Wullamson, A., Wleczyk, R., Wooden, S., Worley, K., Weistock, G., Williamson, A., Wleczyk, R., Wooden, S., Weistock, G., and Gibbs, R.
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/protein_id="AAC14695.1"
/db_xref="GT:2801825"
/db_xref="CT:2801825"
/translation="LQQRINGDESKELPMTTQMSSGNTESPEMRRDSEQHGNGEL
RGMFTINSIGRIGGNWGEYATLEALARNNGRLAFIPASMHNALAPIFRISLVHHSDT
AKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVRE
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125, USA
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Battus norvegicus,
Bukaryosi, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
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                                                                                                                                                               143643 CACCCTICCGGATTCTCCGTCAAAGTCTTAAAGCCAGAGGCAGCCTTCCTACCAGA
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                                                                                                                                             CACCCTTCCGGATTCTCCGTTCCTCAAAGTCTTTAAGCCAGAGGCAGCCTTCCTACCCGA
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Direct Submission
Submitted (13-JAN-1998) Cell Surface Blochem., Nor1
120 Northgate Plaza, Suite 230, Seattle, WA 98125,
Location, Qualifiers
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86101:
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4943. - 4948
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                                                                          linear ROD 26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MASAQVPFSFPLAHFLIFVFVTSTIIHLQQRIVKLQTLSEKELQ
                                                                                                                                                                                        Bukaryota...

Bukaryota...

Mammalia, Butheria, Rodentia, Sciurognathi; Muridae, Murinae; Mus. 1 (bases 1 to 6762)

Domino, S.E., Zhang, L. and Lowe, J.B.

Molecular cloning, genomic mapping, and expression of two secretor blood group alpha (1,2)fucosyltransferase genes differentially regulated in mouse uterine epithelium and gastrointestinal tract J. Biol. Chem. 276 (26), 23748-23756 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="fucosyltransferase; similar to the Mus musculus strain ICR Sec2 sequence deposited at GenBank Accession Number AF064792; similar to the Homo sapiens secretor blood group alpha(1,2) fucosyltransferase FUTZ sequences deposited at GenBank Accession Numbers D87942 and UI7894"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Med
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Domino, S.E. and Lowe, J.B.
Mus musculus alpha(1,2)fucosyltransferase FUT2 (Sec2) genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              University of Michigan, 1150 W. -0650, USA.
                                                                            6762 bp DNA linear ROD 26-
alpha(1,2)fucosyltransferase FUT2 (Fut2) gene,
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   1021 GCAAAAGGAGTCACTTGTTACGTCGCAGGAAGAGCCTTCTGATGGGAA 1068
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2210. .3253
/gene="Fut2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="alpha(1,2)fucosyltransferase FUT2"
/protein_id="AAF45146.1"
/db_xref="GI:7288505"
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/cell_line="E14"
/cell_type="Es"
/cell_type="Es"
/gene="Fut2"
/note="Sec2"
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Direct Submission
Submitted (13-DEC-1999) HHMI, Univer
Ctr. Dr., Ann Arbor, MI 48109-0650,
Location/Qualifiers
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/organism="Mus musculus"
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/db_xref="taxon:10090"
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/gene="Fut2"
                                                                                                                                       AF214656.1 GI:7288504
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3 (bases 1 to 6762)
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                                                                                          DEFINITION
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TITLE
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MEDLINE
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                                                                                                       CAAATGTCCTCGGGAAACACACAGAAAGCCCAGAGATGCGACGGGACCGGGACAGCAGCATGGG 201
                                                                                                                                                                     AATGGAGAGCTGCGGGGCATGTTCACGATCAATTCCATTGGCCGGCTGGGGAACCAGATG 261
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                                                             TACCACCACCTGCGCCCAGAGATCCTGAAGGAGTTCACCCTGCATGACCACGTGCGGGAG
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                 Indels
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            Matches 1068;
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Db 3209 TGGATGGCCATCCCGGAGACCIGTCCCCACTCTTAAGCACTAACAACCAGCTGTCCT 3268 QY 1081 CGGTCCCACTTCCACCTCAAGGCAAAAGGAGTCACTTGTTACGTCGCAGGAAGACCTTT 1140 Db 3269 TGGTCCCATTTCCAAGGCAGAAGGAGTCACTTGGTACATCCCAGGAAGGCCTTC 3328 QY 1141 TGATGGGAA 1149 Db 3329 TACTGGGAA 3337	RESULT 7 AC073774/C LOCUS LOCUS LOCUS DEFINITION MUS musculus clone RP23-36F17, WORKING DRAFT SEQUENCE, 14 ordered ACCESSION AC073774.2 GI:9256789 VERSION AC073774.2 GI:9256789 VERSION AC073774.2 GI:9256789 VERSION AC073774.2 GI:9256789	HTG; HTGS_FHASE2; HTGS_ Mus musculus. Mus musculus. Eukaryota; Metazoa; Cho Mammalia; Eutheria; Rod I (bases 1 to 200146) DOE Joint Genome Institt Sequencing of Mouse	JOURNAL Unpublished REFERENCE 2 (bases 1 to 200146) AUTHORS DOE Joint Genome Institute. TITLE Direct Submission JOURNAL Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 18, 2000 this sequence version replaced gi:8810391.	Center: John Genome Institute Center Code: JGI/www.jgi.doe.gov Project Information Center Project Name: 1750833 Center clone name: RPCI-23_36F17	Summary Statistics Consensus quality: 191947 bases at least 040 Consensus quality: 197212 bases at least 030 Consensus quality: 197212 bases at least 020 Estimated insert size: 236210; agarose-fp estimation Estimated insert size: 199546; sum-of-contigs estimation Quality coverage: 7 3 in 020 bases; agarose-fp estimation Quality coverage: 8.65 in 020 bases; sum-of-contigs estimation.	* NOTE: This is a 'working draft' sequence. It currently * consists of 14 contigs. Gaps between the contigs * are represented as runs of N. The order of the pieces * is believed to be correct as given, however the sizes * of the gaps between them are based on estimates that have * provided by the submittor. * This sequence will be replaced * by the finished sequence as soon as it is available and		* 66983 67082: gap of unknown length * 67083 106953: contig of 39871 bp in length * 107054 11366: contig of 4313 bp in length * 11367 11466: gap of unknown length * 11467 113014: contig of 1548 bp in length * 113015 113114: gap of unknown length
Best Local Similarity 89.7%; Pred. No. 1.3e-238; Matches 1031; Conservative 0; Mismatches 97; Indels 21; Gaps 2; Qy 1 AIGGCCAGGGTCCTTTCTCTTTCTCTGGCCCACTTCTTGTCTT 60 LILLI		QY 241 GGCCGGCTGGGGAACCAGATGGGCGAATACGCCACACTCTTGCACTGGCCAGGATGAAC 300 Db 2429 GGCCGCCTGGGGAACCAGATGGCGAATATGCTTGCACTGGCCAGGATGAAC 2488 QY 301 GGACGCTTGCGTTCATCCCGGCATGCACACCTCTAGGCCCCATCTTCAGGATC 360 Db 2489 GGTCGCTTGCTTCATCCCGGCATGCACACCTCTAGGCCCCATCTTCAGGATC 360 Db 2489 GGTCGCTTGATCCTCATGCACACCACTCTAGGCCCCATCTTCAGGATC 2548	QY 361 AGCCTCCCGGTGTTACACAGCGCAAAAAGATCCCATGGCAGATTACCATCTC 420 Db 2549 AGTCTCCCGGTGTTACACAGCGACACAGAAGGATCCCGTGGCAGAATTACCACCTC 2608 QY 421 AACGACTGGATGGAGAGAGGTTACCGCCACATTCCGGGACACTTTGTGCGCTTCACGGA 480 Db 2609 AACGACTGGATGGAGAGGGTTACCGCCACATCCGGGGCACATTTGTGCGCTTCACGGA 480 Db 2609 AACGACTGGATGGAGGGTTACCGCCACATCCCGGGCCAGTATGTGCGTTTCACGGA 2668	QY 481 TACCGTGCTCTGGACCTTCTACCACCACCACGGGACCTGGAGGAGTTCACC 540 Db 2669 TACCGTGCTCTGGACCTTCTACCACCACCACGGCCCAGAGATCCTGAAGGAGTTCACC 2728 QY 541 CTGCATGACGGGGAGGAGGCCCAGGCCTTCCTGCGTGGTCTCTCGGGTGATGGG 600 Db 2729 CTGCAGGACGTGCGGAGGAGCCCAGGCCTTCCTGCGTGGTCTTCTGCGGGTGAATGGG 2788	OY 601 AGCCAGCCGACTACTTTGTGGGTGTCCATGTGCGCGGGGGCTTTGTGTGCATGTGCATG 660	Oy 721 TTCCGGGCACGCTATTCATCTCCAGCTTTCGTGGTTACAAGCAACGGTATGGCCTGGTGC 780 Db 2909 TTCCGGGCACGCTATTCATCTCCAGTCTTCGTGGTTACAAGCAACGGTATGGCTGGTC 2968 Qy 781 GGGAAAACATTAATGCTTCCGAGACGTGGTGTTCGCGGCAATGGTATTGAGGG 840 Db 2969 GGGAAAACATCAACACCTCCCTAGGACGTGTTTCGCGGGCAATGGTATTGAGGG 840	841 3029 901 3089	961 3149 1021

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Biochim. Biophys. Acta 1487 (2-3), 275-285 (2000)
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mummalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 1044)
Lin, B., Hayashi, Y., Saito, M., Sakakibara, Y., Yanagisawa, M. and Iwamori, M.
                                               841 TCGCCAGCCAAGGACTTCGCGCTGCTCACCCAGTGCAACCACCATCATGACTATTGGG
                           TTCCGGGCACGCTATTCATCTCCAGTCTTCGTGGTTACAAGCAACGGTATGGCCTGGTGC
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Lin.B., Hayashi.Y., Saito,M., Sakakihara,Y., Yanagisawa,M.
Iwamori,M.
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Submitted (12-MAY-1998) Chemistry, Faculty of Selence & T
Kinki University, Kowakae, Higashi-osaka 577-8502, Japan
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/product="GDP-L-fucose:beta-D-galactoside
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Mus musculus GDP-L-fucose:beta-D-galactoside
2-alpha-1-fucosyltransferase mRNA, complete cds.
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/note="sec2; Se"
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1: contig of 4877 bp in length
1: gap of unknown length
2: contig of 28326 bp in length
3: contig of 8071 bp in length
3: gap of unknown length
3: gap of unknown length
2: gap of unknown length
2: gap of unknown length
3: contig of 1835 bp in length
3: contig of 1835 bp in length
3: gap of unknown length
3: gap of unknown length
3: contig of 18505 bp in length
3: contig of 3164 bp in length
3: contig of 3164 bp in length
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52711 c 50595 g 48057 t 1301 oth
                                                                                                                                                                                                                                                                                                                                                                                                                     81.1%; Score 931.8; DB 2;
89.7%; Pred. No. 1.5e-238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-36F17"
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1. .200146
                                                                                                             158642:
158742:
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Mus misculus FUT2 gene for GPP-L-fucose.beta-D-galactoside
2-alpha-1-fucosyltransferase, partial cds, strain:G57BL/10snJ.
AB039114
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/db_xref="GI:15822974"
/translation="FLIFVFVTSTIIHLQQRIVKLQTLSEKELQAVQMSSPNAARTDM
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VLBSTDARRIUMQNYHLNUMDBERYHIPGQYYRTGYPCYSMPYHHERPEILKEFTL
HDHYRDEAQAFLKGIRVNGSQPSTFYGYHYRGDYYRYMYKYWKGYADKGYIEKALD
RFRARYSSPVFVVTSNGMAWGRENINTSLGDVYPAGNUIBGSPAKDFALLTQCHFTIM
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Mus musculus (sub_species:domesticus, strain:C57BL/10SnJ) DNA.
Mus musculus
                            Gene Genealogies of 21 Nuclear Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. (bases 1 to 963)
Liu, Y. and Saitou, N.
Direct Submission
Submitted (29-FEB-2000) Naruya Saitou, National Institute of
Genetics, Laboratory of Evolutionary Genetics; 1111 Yata, Mishima,
Shizuoka 411-8340, Japan (E-mail:nsaitou@genes.nig.ac.jp,
URL:http://sayor.lab.nig.ac.jp/, Tel:81-559-81-6790,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                      880 ACCTTTGGGATTTGGGCTGCCTACCTGGCAGGTGTATACCATCTACCTAGCCAACTAC
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TCGCCAGCCAAGGACTTCGCGCTGCTCACCAGTGCAACCACCACCATCATGACTATTGGG
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285 c 257 g 207 t
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2-alpha-1-fucosyltransferase"
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/organism="Mus musculus"
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/chromosome="7"
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Query Match

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		AB039115.1 G FUT2; GDP-L-F		Mammalia; Eut 1 Liu,Y., Kitan Saiton M	Conspicuous D of Five Mus m Unpublished 2 (bases 1 to	Liu, Y. and Sa Direct Submis Submitted (29 Genetics, Lab	Shizuoka 411- URL:http://sa Fax:81-559-81 Loca	e 1 /org/ /str/	/db_ /chr/ /notv	1/gene/ <1. /gene/	/EC_) /note /code /pro	2-all /pro/ /db_ /tra	QQSAI VLHSI HDHVI RFRAI	TIGT)	Query Match Best Local Similarity Matches 888; Conserva	43 TICCICATCIT 	103 CTCCAACCCCTC	163 GAAAGCCCAGA(
AB039115	LOCUS DEFINITION ACCESSION	VERSION KEYWORDS	SOURCE ORGANISM	REFERENCE AUTHORS	TITLE JOURNAL REFERENCE	AUTHORS TITLE JOURNAL	FEATURES	sourc		gene				BASE COUNT ORIGIN	Query Match Best Local Matches 88	λζο Op	Qy Dp	Qy Dp	» O
Similarity 90.2%; Pred. No. 7.6e-204;	Matches 888; Conservative 0; Mismatches 43 TICCTCAICTTTGTCTTCGTGACTTCCACCATC	1 TICCTCAICTTTGTCTTTGTGACTTCCACCATCACCTCCACCTCCACGAACGA	1	163 GAAAGCCCAGAGATGCGACGGGACAGCATGGGAATGGAGAGCTGCGGGGCATG 222	223 TTCACGATCAATTCCATGGCGGCTGGGGAACCAGATGGGCGAATACGCCACACTTT 2	283	343 GCGCCCATCTTCAGGATCAGCCTCCCGGTGTTACACAGCGACACGGCCAAAAAGATCCCA 402 	403 TGGCAGAATTACCATCTCAACGACTGGATGGAGGGGTTACCGCCACATTCCGGGACAC 462 	463 TTTGTGGGCTTGACGGGATACCCGTGGTCCTGGACCTTCTACCACCACGTGGGCCCAGAG 522	523 ATCCTGAAGGAGTTCACCCTGCATGACCACGTGGGGGGGG	583 GGTCTGGGGGTCAATGGGAGCCGAGTGCTTTTGTGGGTGTCCATGTGGGGGGG 642 	643 GACTATGEGEARGECCEAATGEGGAAGGCGEGGGGGGGGGGGTACCEG 702 	703 GAAAAGGCCCGGATATGTTCCGGGCACGCTATTCATCTCCAGTCTTCGTGGTTACAAGG 762 	763 AACGGTATGGCCTGGTGCCGGGAACATTAATGCTTCCCGAGGAGACGTGGTGTTCGCG 822 	823 GGCAATGGTATTGAGGGGTCGCCAAGGACTTCGCGGTGCTGCTCCACCCAGTGCAACCAC 882		943	GCAGCOTTCCTACCCGAATGGGTG 1026	940 GCAGCCITCCICCCCGAGTGGAIG 963
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AB039115 LOCUS DEFINITION	13 bp DNA linear GDP-L-fucose:beta-D-gala
z	fucosyltransferase, partial cds, strain:BFM/2Ms GI:15822975 L-fucose:beta-D-galactoside 2-alpha-1-fucosyltr us (sub_species:brevirostris, strain:BFM/2Msf)
OKGANISM	ta; Craniata; Vertebrata; ia; Sciurognathi: Muridae:
REFERENCE AUTHORS	tano, T., Koide, T., Shiroishi, T., Moriwaki, K. and
	Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of Five Mus musculus subspecies
JOURNAL REFERENCE	
	ruya Saitou, National Ins Olutionary Genetics; 1111
	z.jp/, Tel:81-559-81
FEATURES Source	Location/Qualifiers 1963
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	/chromosome="7" /note="sequence used for primer design based on
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S(D)	
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	VERMINDER GELEGOT FEBER VER 1511 INDEQNA VERSKERENDER VERSKER VERSKERENDER VERSKERE
	VLRIDALARKALWONI RENDAMBERKIRH PUQIY VETUS PUCAWIFY HELKEFELLKEFT HDHYRERQAFILKGLRYNKSOPSTEVGROYVHYRGDYVHYMKYVWK GVVADRGYLEKALD RFRARXSSPYFVYTSOMAMORRINI MYSLOPYPRAGNGILGSSPAKDFALLTOCNHTYM
BASE COUNT ORIGIN	TIGTEGIWAAYLAGGDTIYLANYTLPDSPFLKIFKPAAAFLPEWM" 214 a 285 c 257 g 207 t
Query Match	69.8%; Score 802; DB 10;
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Qy 4	3 TICCTCATCTTTGTCTTCGTGACTTCCACCATCATCCACCAGCGAGTGAAG 102
qq	1 ITCCICATCITIGICITIGICATICATCATCATCCACCACCACCACGAACGAATAGTGAAG 60
07 10	3 CICCAACCCCTGICAGAAAGAATTACCGAIGACGACTCAAAIGICCTCGGGAAACACA 162
Db da	1 CTCCAAACCCTGTCAGAAGGAATTACAGGCGGTTCAAATGTCCTCACCAAACGCG 117
Qy 16	3 GAAAGCCCAGAGATGCGACGGGACAGCGAGCGCATGGGAATGGAGAGCTGCGGGGATG 222
Db 118	
Qy 22.	m
Db 160	

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VLHSDPARRIPWQWTHJNDWMEBERRHIPGQYVRFTGYPCSWTFYHHLRPEILKEFTL
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FRRARYSSSPYRVTSNGMAMORENINTSLGDVVFAGNGIEGSPAKDFALLTOCNHTIM
TIGTFGIWAAYLAGGDTYLANYTLEDSPFLKIFKPAAAFLPEWM"
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Liu,Y. and Saitou,N.
Direct Submission
Submitsed (29-FEB-2000) Naruya Saitou, National Institute
Genetics, Laboratory of Evolutionary Genetics; 1111 Yata,
Shizuoka 411-8540, Japan (B-mail:nsaitou@genes.nig.ac.jp,
URL:http://sayer.lab.nig.ac.jp/, Tel:81-559-81-6790,
Fax:81-559-81-6799)
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                                                                                                                                                                                                                                                                     /note="sequence used for primer design based Acc#AF064792"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 963;
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Pred. No. 7.6e-204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                      /organism="Mus musculus"
                                                                                                                                                                                          /strain="BLG2/Msf"
/sub_species="musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                     /EC_number="2.4.1.69"
/note="Sec2; Se"
                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                   /chromosome="7
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90.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 GCGCCCATCTTCAGGATCAGTCTCCCGGTGTTACACAGGGACACACAGCCAGAAGGATCCCG
                                                                                                                                                                      TGGCAGAATTACCATCTCAACGACTGGATGGAGGAGCGTTACCGCCACATTCCGGGACAC
                                                                                                                                                                                              643 GACTATGTGCATGTCATGCCTAATGTGTGGAAGGGCGTGGTGGCTGACCGGGGTTACCTG
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                GCGCCCATCTTCAGGATCAGCCTCCCGGTGTTACACAGGGGGACACGGCCAAAAAGATCCCA
                                                                                                                                                                                                                                                 TITGTGCGCTTCACGGGATACCCGTGCTCCTGGACCTTCTACCACCACCTGCGCCCAGAG
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                                                                                                                                                                                                                                                                                                                           ATOCTGAAGGAGTTCACCCTGCATGACCACGTGCGGGAGGAGGCCCAGGCCTTCCTGCGT
                                                                                                                                                                                                                                                                                                                                                               460 ATCCTGAAGGAGTTCACCCTGCACGACCATGTGCGTGAGGAGGCCCAGGCTTTCCTGCGT
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Mammalia; Eutheria; Rodentia; Sciurognat
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SOURCE ORGANISM

COURNAL REFERENCE

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AUTHORS REFERENCE

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DEFINITION

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ACCESSION VERSION KEYWORDS

RESULT 11 AB039116

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Query Match Best Local Similarity 90.2%; Pred. Matches 888; Conservative 0; Mi	Qy	Oy 103 CTCCAACCCCTGTCAGAAGAAT	Qy 163 GAAAGCCCACAGATGCGACGGGACA	QY 223 TICAGGATCAATTCCATTGGCCGGC	OY 283 GCACTGGCCAGGATGAACGGACGCC	Oy 343 GGGCCATCTTCAGGATCAGCCTCC	Qý 403 TGGCAGAATTACCATCTCAAGGACT	540 463	Db 400 IATGTGCGTTTCACGGGATACCGGT	46	Qy 583 GGTCTGCGGGTGAATGGGAGCCAGC		Db 580 GACTATGTGCATGTCCAAGGC	Qy 703 GAAAAGGCCTGGATATGTTCCGGGC	763	700	Qy 823 GGCAATGGTATTGAGGGGTCGCCAGG	Db 760 GGCAATGGTATTGAGGCTCACCAGG	4y 883 ACCAICATGACTATTGGGACCTTTGC		088	OY 1003 GCAGCCTTCCTACCCAARGGGGG 1
823 GGCAATGGTATTGAGGGTCGCCAGCCAAGGACTTCGCGCTGCTCACCCAGTGCAACCAC 882 	ACCATCATGACTATTGGGACCTTTGGGATTTGGGCTGCCTGC	01	GCAGCCTTCCTACCCGAATGGGTG 1026		AB039118 Mus musculus FUT2 gene for GDP ⁻ L-fucose:beta-D-galactoside 2 Alpha-1-fucosyltransferase, partial cds, strain:MSM/Msf.	AB039118.1 GI:15822981 FUT2; GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase. Mus musculus (sub_species:molossinus, strain:MSM/Msf) DNA. Mus musculus	ia; Metazoa; Chordata;	Liu, Y., Kitano, T., Koide, T., Shiroishi, T., Moriwaki, K. and Saitou, N. Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes	Oppublished and subspecies 2 (bases 1 to 963)	Liu,Y. and Saitou,N. Direct Submission Submitted (29-FFR-2000) Nariuma Saiton, National Tratitude of	Genetics, Laboratory of Evolutionary Genetics; 1111 rata, Mishima, Shizuoka 411-8540, Japan (E-mail:nsaitou@genes.nig.ac.jp, UKL.http://syper.lab.nig.ac.jp/, Tel:81-559-81-6790,	rax:01-039-81-0/89) Location/Qualifiers 1963	ulus	/sub_species="molossinus" /db_xref="taxon:10090" /chromosome="taxon"	/hote="sequence used for primer design based on AccaMP064792"	/gre="FUT2" /1>963 <1>963	/gene="FUT2" /BC_number="2.4.1.69"	/note="Sec2; Se" /codon_start=1	/product="GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase" /protein.id="BAB68642.1"	/ub_xrei="Gi:13822982" /translation="FLIFVFVFXIIHLQQRIVKLQTLSEKELQAVQMSSPNAARTDM QQSAKLQGIFTINSIGRLGNOMGEYATLFALARMNGRLAFIPESMHNALAPIFRISLP	VLRSJIARKILFWON HILNDAMBERY RHIPGOYVRFIGYPCSWTFYHHLRPEILKEFTL HDHVREEAQAFLEGLRVNGSQPSTFYCKYHVRKODY VHWRYWKKYWKYVRXYNDROYTEKALD RFRARYSCSVFFYNTMSMCKARTODBY YMGY ON THE AMERICAL OF THE AMERICAN OF THE AMERICA	IIGTFGIWAAYLAGGDIIYLANYTLPDSPFLKIFKPAAFLDEWM" 214 a 285 c 257 g 207 t
QY	QY Db	Qy Db	Qy 1 Db	RESULT 13	LOCUS DEFINITION	VERSION KEYWORDS SOURCE ORGANISM	REFERENCE	AUTHORS	JOURNAL	AUTHORS TITLE JOURNAL		FEATURES Source			G G G	CDS						BASE COUNT ORIGIN

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                                                     NTTACCGATGACGACTCAAATGTCGTCGGGAAACACA
                                                                                           AGCGAGCAGGAATGGAGAGCTGCGGGGCATG
                                                                                                                                                             CTGGGGAACCAGATGGGCGAATACGCCACACTCTTT
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                    21;
Length 963;
                    75; Indels
 re 802; DB 10;
1. No. 7.6e-204;
                     Mismatches
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ATCIACTTAGCCAACTACACCCTTCCGGATTCTCCGTTCCTCAAAGTCTTTAAGCCAGAG 1002
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Mus musculus (sub_species:molossinus, strain:SWN/Msf) DNA.
Mus musculus
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of Five Mus musculus subspecies
Unpublished
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                                                               TATGIGGATICACGGGATACCCGIGCTCTGGACCTTCTACCACACGTGCGCCAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      403 TGGCAGAATTACCATCTCAACGACTGGATGGAGGGAGCGTTACCGCCACATTCCGGGACAC
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Sciurognathi; Muridae;
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Mammalia; Butheria; Rodentia;
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                                                                                                                                                                     FUT2; GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase.
Mus musculus (sub_species:domesticus, strain:pgn2) DNA.
Mus musculus
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Mishima,
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                                                                                                                                                                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (29-FEB-2000) Naruya Saitou, National Institute Genetics, Laboratory of Evolutionary Genetics; 1111 Yata, Shizuoka 411-8540, Japan (E-mail:nsaitou@genes.nig.ac.jp, URL:http://sayer.lab.nig.ac.jp/, Tel:81-559-81-6790, Fax:81-559-81-6789)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="sequence used for primer design based on Acc#AF064792"
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/organism="Mus musculus"
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of Five Mus musculus subspecies
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                                                                         Mus musculus FUT2 gene for
                                                                                                                                           AB039119.1 GI:15822983
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/gene="FUT2"
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Liu, Y. and Saitou, N.
Direct Submission
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2-alpha-1-fucosyltransferase"
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RFRARXSSPVFVYTSNGMAWCRENINTSLGDVVFAGNGIEGSPAKDFALLTQCNHTIM
TIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKIFKPAAAFLPEWM"
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Mishima,
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2 (bases 1 to 963)
Liu,Y. and Saitou,N.
Direct Submission
Submitted (29-FEB-2000) Naruya Saitou, National Institute of Genetics, Laboratory of Evolutionary Genetics; 1111 Yata, PShizuoka 411-8540, Japan (E-mail:nsaitou@genes.nig.ac.jp, URL:http://sayer.lab.nig.ac.jp/, Tei:81-559-81-6790,
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/organism="Mus musculus"
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/note="Sec2; Se"
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                                                                                                                                                                                                                                                                     Acc#AF064792"
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/gene="FUT2"
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(without alignments)
8682.922 Million cell updates/sec
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GenCore version
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ALIGNMENTS

AAC67965 standard; cDNA; 1149 BP.

RESULT 1 AAC67965 19-FEB-2001

AAC67965;

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Rat; alphal-2fucosyltransferase; cytostatic; neuroprotective; nootropic; gene therapy; Fucalphal-2calbetal-3GalNAc; immunotherapy; immunosuppression; cancer; neurological disease; small cell lung carcinoma; ss.
                                                     H35 cell alphal-2fucosyltransferase cDNA.
                                                                                                                                                                                                                                  ---
                                                                                                                                                                                                              (PACI") PACIFIC NORTHWEST CANCER FOUND.
                                                                                                                                                                            99WO-US07384.
                                                                                                                                                                                             99WO-US07384.
                                    (first entry)
                                                                                                                                                                                                                                 Holmes EH, Sherwood AL;
                                                                                                                                                                                                                                                   WPI; 2000-687262/67.
P-PSDB; AAB36104.
                                                                                                                     Rattus norvegicus
                                                                                                                                      WO200064464-A1.
                                                      Rat hepatoma
                                                                                                                                                                           23-APR-1999;
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                                                                                                     The present sequence is given in a specification relating to a rate ganglioside GM_1-specific alphal-2fucosyltransferase protein. The protein or its cellular fraction is useful for synthesis of a molecule comprising Fucalphal-3dalbetal-3dalNac. a glycolipid, glycoprotein, glycolipoprotein or a free oligosaccharide comprising Fucalphal-2dalbetal-3dalNac. The method involves contacting alphal-2fucosyltransferase with GDP-fucose and a molecule or glycolipid, glycoprotein, glycolipoprotein or oligosaccharide having a terminal Galbetal-3dalNac group. It is also oligosaccharide having a terminal Galbetal-3dalNac group. It is also useful for synthesis of fucosyl-GM_1 by contacting the protein with GDP-fucose and ganglioside GM_1. The obtained glycoproteins, glycolipids and cligosaccharides are useful as nutritional compositions and fucosyl-GM_1 is useful for inducing an immunotherapeutic or immunosuppressive action against cancer,
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New rat ganglioside GMI-specific alphal-2Fucosyltransferase, useful for preparation of fucosyl GMI which is useful as a nutritional composition or immunotherapeutic for cancer and neurological diseases -
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                                                                     Claim 10; Fig 5; 91pp; English
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                                                                                                                                        ACCITIGGGATTIGGGCTGCCTACCTGGCAGGTGGTGATACCATCTACTTAGCCAACTAC
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                                                                         CGGGAGAACATTAATGCTTCCCGAGGAGACGTGTGTTCGCGGGCAATGGTATTGAGGGG
                                                                                                                          TCGCCAGCCAAGGACTTCGCGCTGCTCACCCAGTGCAACCACCATCATGACTATTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat; alphal-2fucosyltransferase, alphal-2fucT; antisense therapy; galactose betal-3favectylgalactosamine; Galbetal-3faslNac; glycolipid; glycoptotein; ollgosaccharide; fucosyl-GM; cancer; gene therapy; oncogenic transformation; cytostatic; ganglioside; GMI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hepatoma H35 cell alphal-2FucT"
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1..1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD27207 standard; DNA; 1149 BP.
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/product=
662..1149
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for producing

The invention relates to rat GMI-specific alphal-2fucosyltransferase
(alphal-2FucT) enzyme and its corresponding nucleic acid. This nucleic
acid is specific for a carbohydrate molety found in ganglioside GMI,
a terminal galactose betal-1N-acetylgalactosamine (Galbetal-3GalNAc)
acchaide. Alphal-2FucT DNA is useful for producing rat alphal-2FucT
protein by recombinant techniques. Alphal-2FucT DNA is useful for the
preparative synthesis of fucosyl containing glycolipids, glycoproteins,
glycolipoproteins and oligosaccharide, and for preparing fucosyl-GMI.
Alphal-2FucT DNA is useful for detecting oncogenic transformation which
involves assaying for changes in expression of alphal-2 FucT. Since
alphal-2FucT is activated in cell transformation, antisense sequences
dcrived from alphal-2FucT DNA is useful in gene therapy and
cor treating cancer. Alphal-2FucT DNA is useful in gene therapy and Rat hepatoma H35 cell alphal-2fucosyltransferase, useful for producing GMI-specific alphal-2fucosyltransferase enzyme by recombinant techniques and for detecting oncogenic transformation of test tissues AACGACTGGATGGAGGAGCGTTACCGCCACATTCCGGGACACTTTGTGCGCCTTCACGGGA Claim 1; Fig 5; 41pp; English. Best Local Similarity 100. Matches 1149; Conservative 2002-121132/16 alphal-2FucT DNA P-PSDB; AAE16622 361 Query Match 61 181 181 241 241 301 301 361 421 421 Ωğ QQ Q QQ QΩ qq g g q δ ò ά δŏ δã ã ŏ δŽ

Sequence 1149 BP; 247 A; 341 C; 311 G; 250 T; 0 other;

ö Gaps ., DB 24; Length 1149; Indels 100.0%; Score 1149; DB 24; 100.0%; Pred. No. 1.8e-310; . 0 0; Mismatches

GIGACTICCACCATCATCCACCICCAGCAGCGAATAGIGAAGCICCAACCCCTGICAGAG 1 AIGGCCAGCCCCAGGIICCTTTCTCCTTTCCTCTGCCCCACTICCTCATCTTTGTCTTC

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180 240 240 CGGGACAGCGAGCAGCAIGGGAAIGGAGAGCTGCGGGGGCAIGIICACGAICAATICCAIT CGGGACAGCGAGCAGCATGGGAATGGAGGCTGCGGGGGCATGTTCACGATCAATTCCATT

GGCCGGCTGGGGAACCAGATGGGCGAATACGCCAACACTCTTTGCACTGGCCAGGATGAAC GGCCGGCTGGGGAACCAGATGGGCGAATACGCCACACTCTTTGCACTGGCCAGGATGAAC

300 300

360 360 GGACGGCTTGCGTTCATCCCCGCATCCATGCACACGCTCTAGCGCCCATCTTCAGGATC

420 420 AGCCTCCCGGTGTTACACACGCGACACGGCCAAAAAAATCCCATGGCAGAATTACCATCTC

480 540

TACCCGTGCTCCTGGACCTTCTACCACCTGCGCCCCAGAGATCCTGAAGGAGTTCACC TACCCGTGCTCCTGGACCTTCTACCACCTGCGCCCAGAGATCCTGAAGGAGTTCACC 481 481

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AAC67966 standard; cDNA; 1068 BP (first entry) 19-FEB-2001 AAC67966; AAC67966 RESULT

Rat hepatoma H35 cell alphal-2fucosyltransferase catalytic domain cDNA Rat; alphal-2fucosyltransferase; cytostatic; neuroprotective; nootropic; gene therapy; Fucalphal-2Calbetal-3GalNAc; immunotherapy; immunosuppression; cancer; neurological disease; cell lung carcinoma; ss.

Rattus norvegicus

WO200064464-A1.

02-NOV-2000

99WO-US07384, 99WO-US07384 23-APR-1999; 23-APR-1999; (PACI-) PACIFIC NORTHWEST CANCER FOUND

AL; Holmes EH, Sherwood

900

WPI; 2000-687262/67. P-PSDB; AAB36105. New rat ganglioside GMI-specific alpha1-2Fucosyltransferase, useful for preparation of fucosyl GMI which is useful as a nutritional composition

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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                               The present sequence is given in a specification relating to a rat gauglioside GM 1-specific alphal-2fucosyltransferase protein. The protein or its cellular fraction is useful for synthesis of a molecule comprising Fucalphal-2Gabbetal-3GalNac, a glycolipid, glycoprotein, glycolipid or a free oligosacharide comprising Fucalphal-2Gabbetal-3GalNac, and a molecule or glycolipid, glycoprotein, glycolipoprotein or and a molecule or glycolipid, glycoprotein, glycolipoprotein or oligosaccharide having alphal-2fucosyltransferase with GDP-fucose unseful for synthesis of fucosyl-GM_1 by contacting the protein with GDP-fucose and ganglicate GML. The obtained glycoproteins, glycolipids and cligosaccharides are useful as nutritional compositions and fucosyl-GM_1 is useful for inducing an immunotherapeutic or immunosuppressive action against cancer, neurological disease or small cell lung carcinoma.
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                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                        93.0%; Score 1068; DB 21; Length 1068; 100.0%; Pred. No. 7.3e-288;
immunotherapeutic for cancer and neurological diseases
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                                                                                                                                                                                                   Sequence 1068 BP; 237 A; 308 C; 300 G; 223 T; 0 other;
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                    Claim 11; Fig 3A; 91pp; English.
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Matches 1068; Conserv
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/product= "Rat hepatoma H35 cell alphal-2FucT catalytic
                       for producing
CTGCTCACCCAGTGCAACCACCACCATGACTATTGGGACCTTTGGGATTTGGGCTGCC
                                                                                                                            TACCTGGCAGGTGGTGATACCATCTACTTAGCCAACTACACCCTTCCGGATTCTCCGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain"
/note= "CDS does not include start codon'
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The invention relates to rat GMI-specific alphal-2fucosyltransferase (alphal-2FucT) enzyme and its corresponding nucleic acid. This nucleic acid is specific for a carbohydrate molety found in ganglicaside GMI, a terminal galactose betal-3W-acetylgalactosamine (Galbetal-3GalNAc) saccharide. Alphal-2FucT DNA is useful for producing rat alphal-2FucT protein by recombinant techniques. Alphal-2FucT DNA is useful for the preparative synthesis of fucosyl containing glycolipids, glycoproteins, glycolipoproteins and oligosaccharide, and for preparing fucosyl-GMI.

Alphal-2FucT DNA is useful for detecting oncogenic transformation which involves assaying for changes in expression of alphal-2 FucT since alphal-2FucT DNA is useful for detecting oncogenic transformation which involves assaying for changes in expression of alphal-2 FucT since alphal-2FucT DNA are useful for inhibiting, suppressing cor treating cancer. Albhal-2FucT DNA is useful in gene therapy and antisense therapy. The present sequence is rat hepatoma H35 cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TACCACCACCTGCGCCCCAGAGATCCTGAAGGAGTTCACCCTGCATGACCACGTGCGGGAG 561
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Claim 2; Fig 3; 41pp; English.
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Matches 1068; Conservative
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1101 960 CTGTCCCCACTCCTTAAGGCATTAACACCAGCCTGTCCTGGGTCCCACTTCCACCTCAAG 961 CIGICCCCACICCITAAGGCALTAACACCAGCCIGICCICGGICCCACTICCACCICAAG CTGCTCACCCAGTGCAACCACACCATCATGACTATTGGGAACCTTTGGGATTTGGGCTGCC CIGCTCACCCAGTGCAACCACCATCATGACTATTGGGACCTTTGGGATTTTGGGCTGCC TACCTGGCAGGTGATACCATCTACTTAGCCAACTACACCCTTCCGGATTCTCCGTTC TACCTGGCAGGTGGTGATACCATCTAGTTAGCCAACTACACCCTTCCGGAITCTCCGTTC enzyme This nucleotide sequence, designated clone pSe16.1, codes for porcine secretor (Se) glycosyltransferase (see AAM7885), an enzyme that has high affinity for type I and type III substrates. It was isolated from a pig liver genomic library using full-length human Se2 (FUT2) cDNA as probe. The nucleotide sequence shows about 36% nucleic acid, such as porcine Se nucleic acid, into a tissue results in reduced expression of unwanted carbohydrate epitopes on GCAAAAGGAGTCACTTGTTACGTCGCAGGAAGAGCCTTCTGATGGGAA 1149 Nucleic acid encoding glycosyltransferase able to compete with second such enzyme - particularly used to reduce expression of unwanted carbohydrate epitope(s) on tissues intended for 1021 GCAAAAGGAGTCACTTGTTACGTCGCAGGAAGAGCCTTCTGATGGGAA 1068 Secretor; glycosyltransferase; FUI2; pig; epitope; antigen; transgenic animal; xenotransplantation; organ transplant; s Porcine secretor transferase (FUT2) gene. Location/Qualifiers Claim 6; Fig lA-B; 40pp; English. BP AAV29003 standard; DNA; 1043 97WO-AU00540. 96AU-0001823 (first entry) ø Sandrin MS (AUST-) AUSTIN RES INST. .1031 WPI; 1998-169148/15. P-PSDB; AAW37855 transplantation McKenzie IFC, WO9807837-A1 23-AUG-1996; 22-AUG-1997; 28-AUG-1998 26-FEB-1998 Sus scrofa 781 841 901 1042 1102 721 982 862 AAV29003; second RESULT 5 AAV29003 δŏ q δŽ g ŏ qq δŏ q δŏ ö 240 141 120 180 360 201 261 321 441 999 381 501 521 681 900 741 801 09

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                                                                                                                                                                                                                                                                                                                                                                          Gaps
the tissue, especially porcine heart, liver, kidney or pancreas, rendering it more suitable for transplantation, i.e. less immunogenic and of increased immunological acceptability. A claimed method of producing a cell from a donor species that is immunologically acceptable to a recipient species involves reducing levels of carbohydrate on the donor cell that causes it to be recognised as non-self by the recipient by causing a nucleic acid for a glycosyltransferase such as Se to be expressed in the cell. Expression units, such as retroviral packaging or produce cells, containing Se nucleic acids can be used in gene therapy.
                                                                                                                                                                                                                                                                                                                  Score 630.2; DB 19; Length 1043:
Pred. No. 1.1e-165;
0; Mismatches 203; Indels 42;
                                                                                                                                                                                                                                                                     Sequence 1043 BP; 189 A; 352 C; 306 G; 196 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                       54.8%;
76.9%;
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Matches 814; Conservative
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326 GGACGCCTTGCGTTCCATCCCGCATCCATGCACACGCTCTAGCGCCCCATCTTCAGGATC 350 GGCCGGCTGGGGAACCAGATGGGCGAATACGCCAACTCTTTGCACTGGCCAGGATGAAC GCCGCCTGGGGGAACCAGATGGGGGAGTACGCCACCTGTACGCGCTGGCCAGGATGAAC GGGGGGCGGCCTTCATCCCGCCCGAGATGCACAGCACGCTGGCCCCCATCTTCAGGATC 173 207 267 301

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CCTAATGTGTGGAAGGGCGTGGTGGCTGACCGGGGTTACCTGGAAAAGGCCCTGGATATG CCCAACGTGTGGAAGGCGTGGTGGCCGACCGGCGGTACCTGGAGCAGCCCTGGACTGG 627 661

AGCCGACCGAGTACCTACGTGGGGGTGCACGTGCGCGGGGGGGACTACGTGCACGTGATG

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THOCGGGCTCGCTACCGCTCCCCCGTCTTTGTGTCTCCAGCAACGGCATGCCTGGTGT CGGGAGAACATTAATGCTTCCCGAGGAGGACGTGGTGTTCGCGGGCAATGGTATTGAGGGG 687 781

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ITCCGGGCACGCTATICATCICCAGTCTTCGTGGTTACAAGCAACGGTATGGCCTGGTGC 780

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ACCCITCCGGATICICCGITCCTCAAAGICITTAAGCCAGAGGCAGCCTTCCTACCCGAA 1020 TOGCCAGCCAAGGACTTCGCGCTGCTCACCCAGTGCAACCACCATCATGACTATTGGG ACGITCGGGAICIGGGCCGCCTACCITGCTGGTGGAGAGACCAICTACCTGGCCAAITAC ACCITIGGGATITIGGGCTGCCTACCTGGCAGGTGGTGATACCATCTACTTAGCCAACTAC TGGGTGGGCATCCCTGCCGATCTGTCCCCACTCCTTAAG 1059 807 867 927 841 901 1021 g qq ŏ ŏ ŏ

chimeric; glycosyltransferase; gene therapy; AAV21639 standard; cDNA; 1043 encoding cDNA. (first entry) transplantation; ss. secretor; Pig secretor 08-JUL-1998 AAV21639

RESULT 6 AAV21639

Sus scrofa

"secretor" Location/Qualifiers /product= ø 9..1031 /*tag=

WO9805768-A1

96AU-0001402. 97WO-AU00492 96US-0024279 01-AUG-1997; 21-AUG-1996; 02-AUG-1996; 12-FEB-1998

MS: (AUST-) AUSTIN RES INST Sandrin WPI; 1998-159170/14. McKenzie IFC,

P-PSDB; AAW53101

909 009

Nucleic acids encoding chimeric glycosyltransferases - used for altering carbohydrate levels on the surface of cells, useful in therapy and transplantation

Example 2; Fig 6; 51pp; English.

The present sequence encodes pig secretor used in an example of the present invention. The present invention describes nucleic acids (NA) encoding a chimeric glycosyltransferase. The NAS comprise a caralytic domain of a first glycosyltransferase (GT) and a localisation signal of a second GT, whereby when the NA is expressed in a cell and where the chimeric enzyme is located in a marea of the cell where it is able to compete for substrate with a second GT, resulting in reduced levels of a product from the second GT. The NAS can be used to produce cells and organs with desired glycosylation patterns. Products and methods of the epitopes in cells, tissues or organs which may be used in transplantation or gene therapy.

Seguence 1043 BP; 189 A; 352 C; 306 G; 196 T; 0 other;

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69 CACCATCACCTCCAGCACCAGCAATAGTGAAGCTCCAACCCCTGTCAGAGAAGTT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence encodes the human Sec2 protein of the invention. The DNA encodes a alpha(1,2) fucosyltransferase and is the Secretor alpha(1,2) fucosyltransferase locus, that cross hybridises with the H blood group alpha(1,2)fucosyltransferase gene. The DNA is useful for producing a recombinant human GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase (FUT2) which can be used for genotyping an individual as a secretor or nonsecretor as it is known that nonsecretors homozygous for a mutant allale of the FUT2 gene that has a stop codon in the position corresponding to amino acid 143.
                                                                                                                                                                                                                                Sec2; alpha(1,2) fucosyltransferase, H blood group; secretor genotyping; GDP-L-fucose:beta.D-galactoside 2-alpha-L-fucosyltransferase; human; FUT2; nonsecretor genotyping; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 CGCCCAGGTTCCTTTCTCCTCTGGCCCACTTCCTCATCTTTGTCTTCGTGACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   recombinant enzyme and genotyping person as secretor or nonsecretor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoding fucosyltransferase enzyme - useful for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.4%; Score 613.8; DB 19; Length 74.7%; Pred. No. 5.7e-161;
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                TGGGTGGGCATCCCTGCCGATCTGTCCCCACTCGTTAAG 1059
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64..1095
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                                                                                                                                                                                                   Human Sec2 coding sequence.
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nes 813; Conservative
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P-PSDB; AAW69332.
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KELLY R J.
LENNON G.
LOWE J B.
ROUQUIER S.
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                                                                                                    ATGCTCAGCATGCAGGCATCCTTCTTCCCCCACGGGTCCCTTCATCCTCTTTGTCTTC
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                                           Indels
              DB 19;
           Score 630.2; DB 19;
Pred. No. 1.1e-165;
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stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
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                                Lung cancer
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                           Gregaagegeregregeceaccecearaceraceaecageceregacregreeges 806
                                                                                                                        The present invention describes a method (MI) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL7010), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid,
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GATCTGGGCCGCATACCTCACGGGCGGAGACACCATCTACCTGGCCAAITACACCTCCC 1046 1047 CGACTCCCCTTTCCTCAAAATCTTTAAGCCAGAGGCAGCCTTCCTGCCGGAGTGGACAGG 1106 GATTGCCGCAGACCTGTCCCCCTTACTCAAGCACTAATGCTGGCCCATTCTTTGAGACCT 1166 stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma; ACGCTATTCATCTCCAGTCTTCGTGGTTACAAGCAACGGTATGGCCTGGTGCCGGGAGAA CATTGACACCTCCCACGGTGATGTGGTGTTTGCTGGCGATGGCATTGAGGGCTCACCTGC CAAGGACTTCGCGCTGCTCACCCAGTGCAACCACCATCATGACTATTGGGACCTTTGG CAAAGATTTTGCTCTACTCACACAGTGTAACCACACATCATGACCATTGGGACGTTCGG GATTTGGGCTGCCTACCTGGCAGGTGGTGATACCATCTACTTAGCCAACTACACCCTTCC CATCCCTGCCGATCTGTCCCCACTCCTTAAGGCATTAACACCAGCCTGTCCTCGGTCCCA CATTAATGCTTCCCGAGGAGACGTGGTGTTCGCGGGCAATGGTATTGAGGGGTCGCCAGC cancer; colon; breast; ovary; oesophagus; kidney; thyroid; SEQ ID NO:4648. Lung cancer related gene sequence BP CITCCACCTCAAGGC 1103 2000US-233617P. 2000US-234009P. 2000US-234034P. 2000US-234052P. 2000US-235082P. 2000US-235134P. 2000US-235280P. 2000US-235637P. 2000US-235638P. 2000US-235711P. 2000US-235720P. 2000US-235840P. 2000US-209473P. 2000US-209531P. 2000US-233133P. ABL66311 standard; DNA; 3088 2000US-234509P. 2000US-234567P. 2000US-234923P. 20000S-234924P. 20000S-235077P. (first entry) TTTCTCCTTCTCC WO200194629-A2. 18 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 22 - SEP - 2000; 25 - SEP - 2000; 26-SEP-2000; 27-SEP-2000; 27-SEP-2000; 27-SEP-2000; 05-JUN-2000; 18-SEP-2000; 15-MAY-2002 13-DEC-2001 1029 1107 ABL66311; gene; ds. 729 807 867 927 987 789 849 606 1089 Human; Homo RESULT 9 ABL66311 g QΫ́ Db ŏ ΩD Qγ Db δŽ QΩ δy g

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Page 10

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Pancreas cancer related gene sequence SEQ ID NO:8363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACCATCATCCACCTCCAGGAGGAGGTGAAGCTCCAACCCCTGTCAGAAGAAGTT 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oescophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal can infiltrating local cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.3%; Score 612.6; DB 24; Length 3088; larity 73.8%; Pred. No. 1.4e-160; Conservative 0; Mismatches 254; Indels 33;
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2000US-236034P-
2000US-236011P-
2000US-236812P-
2000US-237172P-
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03-0CT-2000; 20000S-237606P.
03-0CT-2000; 2000US-237608P.
01-NOV-2000; 2000US-244867P.
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2000US-236028P.
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29-SEP-2000;
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20-SEP-2000;
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                                              13-DEC-2001
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2000US-235863P

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2000US-236033P 2000US-236109P. 2000US-236111P. 2000US-237173P. 2000US-237278P. 2000US-237294P.

2000US-237295P

2000US-236842P

2000US-237425P.

2000US-237606P. 2000US-237608P.

2000US-237604P

Human; cancer; colon; breast; ovary; oesophagus; kidney; thyrold; stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma; colon; breast; WO200194629-A2 sapiens. Homo

Sequence 3088 BP; 723 A; 839 C; 798 G; 728 T; 0 other; 550505050505050x

2000US-209473P. 2000US-209531P. 2000US-233133P.

2000US-234009P. 2000US-234034P.

2000US-234052P

2000US-233617P

2000US-234509P. 2000US-234567P.

20000S-234923P 2000US-234924P 2000US-235077P 2000US-235082P

2000US-235134P. 2000US-235280P.

2000US-235637P 5638P

20000S-235 20000S-235

carcinoma, papillary carcinoma and Wilm's tumour.

expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110). Or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a structure and/or properties of the agent. MI can be used in the reatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating ductal cancer, infiltrating cancer, infiltrating cancer, infiltrating ductal cancer, infiltrating ductal cancer, infiltrating cancer, infiltrating ductal cancer, infiltrating cancer.

386 446 428 488 566 686 999 89 9 CGCCCAGGTTCCTTTCTCCTTTCCTCTGGCCCACTTCCTCATCTTTGTCTTCGTGACTTC 120 cerreagarecerrecerrecearesceaectrearecrerratescerre CACCATCATCCACCTCCAGCAGCGAATAGTGAAGCTCCAACCCCTGTCAGAGAAGTT TGCGTTCATCCCCGCATCCATGCACAACGCTCTAGCGCCCATCTTCAGGATCAGCCTCCC GGTGTTACACAGGGACACGGCCAAAAAGATCCCATGGCAGAATTACCATCTCAACGACTG GGTGCTGCACAGGGCCACGGCCAGGATCCCCTGGCAGAACTACCACCTGAACGACTG GATGGAGGAGGGTTACCGCCACATTCCGGGACACTTTGTGCGCTTCACGGGATACCCGTG GATGGAGGAGGAATACCGCCACTTCCCGGGGGAGTACGTCCGCTTCACCGGCTACCCCTG CTCCTGGACCTTCTACCACCACCTGCGCCCAGAGATCCTGAAGGAGTTCACCCTGCATGA GAGTACTTTTGTGGGTGTCCATGTGCGCCGAGGGGACTATGTGCATGTCATGCTAATGT 129 ACCGATGACGACTCAAATGTCCTCGGGAAACACAGAAAGCCCAGAGATGCGACGGGACAG 240 GCAGATACCAGTGCTAGCCTCAACATCAAAGGCACTGGGACCCA-------CGAGCAGCATGGGAATGGAGGGTGCGGGGCATGTTCACGATCCAATTCCATTGGCCGGCT DB 24; Length 3088; .4e-160; es 254; Indels 0; Mismatches 53.3%; Score 612.6; 73.8%; Pred. No. 1.4 Best_Local Similarity 73.8
Matches 808; Conservative 180 189 284 447 69 387 Query Match Best Local S 309 369 507 489 567 549 609 327 429 ŏ g ŏ ద ŏ g ŏ q ŏ a ŏ q Qχ g QΫ́ q \overline{Q} g $^{\circ}$ qq Ω

> Horrigan Endress G, Ebner R, KC, Carter Augustus M, Weaver 2; Young PE, 1 Soppet DR,

WPI; 2002-188264/24.

Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene Claim 1; SEQ ID 8363; 44pp; English

728

GTGGAAGGCCGTGGTGGCTGACCGGGGTTACCTGGAAAAGGCCCTGGATATGTTCCGGGC

687 699 747

a ά a 866

ACCCTATTCATCTCCAGTCTTCGTGGTTACAAGCAACGGTATGGCCTGGTGCCGGGAGAA 807 TCGCTACACCTCCCTCATCTTCGTGGTCACCAGTAATGGCATGGCCTGGTGGGGGAGAA

729

The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in

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                                                                                                                                                                                                                               GATTGCCGCAGACCTGTCCCCCTTACTCAAGCACTAATGCTGGCCCATTCTTTGAGACCT 1166
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                            926
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                                                                                                                          GATCTGGGCCGCATACCTCACGGGGGGGACACCATCTACCTGGGCCAATTACACCCTCCC
                                                                                                                                                                    CAAGGACTTCGCGCTGCTCACCCAGTGCAACCACCATCATGAACTATTGGGACCTTTGG
                                                             CATTAATGCTTCCCGAGGAGACGTGGTGTTCGCGGGCAATGGTATTGAGGGGTCGCCAGC
                                                                                                   GATITGGGCTGCCTACCTGGCAGGTGGTGATACCATCTACTTAGCCAACTACACCTTCC
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, useful in gene
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compete for substrate with a second GT, resulting in reduced levels of a product from the second GT. The NAs can be used to produce cells and organs with desired glycosylation patterns. Products and methods of the present invention can be used to reduce the levels of undesirable epitopes in cells, tissues or organs which may be used in
                                                                                                                                                                                                             GCICTAGCGCCCATCTTCAGGATCAGCCTCCCGGTGTTACACAGGGACACGGCCAAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              475 GAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGG
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                                                                         transplantation or gene therapy.
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                                     GGACACTITIGIGGGCTTCACGGGATACCCGTGCTCCTGGACCTTCTACCACCACCTGCGC
                                                                GAGCCCTGGCTGAAGCTCACGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCACCTCCGG
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                                                                                                                                                                                                Swine alpha(1,2) fucosyltransferase; FUT1; Escherichia coli; resistant; E. coli-associated intestinal disorder; E coli infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes swine alpha(1,2) fucosyltransferase (FUT1). The specification describes methods relating to Escherichia coli-resistant swine. One of the methods for identifying a swine resistant to E. coli-associated intestinal disorders, comprises determining whether the base at 307 of alpha(1,2) fucosyltransferasel gene (FUT1) is adenine (Sic), in which case the swine are resistant. The reatment of swine having E. coli-associated disease. The methods can also be used in breeding programmes to identify swine with resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGCTGGCCCTGGCGCGCGCGCGCGCGGCCTTCATCCACCGCGCCATGCACGCC
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                                                                                                                                                            Fragment of pHT83xF encoding swine alpha(1,2) fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.9%; Score 423.8; DB 20; Length 1269; 69.6%; Pred. No. 5e-108; ative 0; Mismatches 252; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diseases - using PCR-RFLP to assay for polymorphisms in the alpha(1,2) fucosyltransferase 1 gene
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/*tag= a
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                                               AAX15872 standard; DNA; 1269
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                                                                                                                         (first entry)
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Best Local Similarity 69.6
Matches 591; Conservative
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                                                                                                                         13-MAY-1999
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                                                                                                                                                                                                                                                         Synthetic
                                                                                    AAX15872;
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/transl_except= (pos:726..728,
replace(315,A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pig alpha-1-2 fucosyltransferase FUT1 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coli; resistance;
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                                                                                                                                                                                                                                                                                              resistant to intestinal colonisation by E. coli. The method comprises determining whether a genetic polymorphism associated with resistance to colonisation is present in a swine sample, and then inferring that the swine is resistant if it is homorphism associated with resistance to colonisation is present is the swine sport the polymorphism. The method enables the breading of present sequence encodes swine FOTI. The method enables the breading of swine that are resistant to E. coli-related diseases. This method comprises breeding swine that have a genetic polymorphism in the FUTI gene. Nor particularly, the identification method identifies swine that are resistant to E. coli-related intestinal disorders if, in a sample taken, the only nitrogen base at residue 30? in the FUTI gene is adening the assay can be used for RFLP analysis, and the assay itself is used as a basis for a kit, applied to swine of any age, in detecting polymorphisms associated with E. coli F18 receptors. The polymorphisms are useful in developing drugs to treat swine with E. coli-related diseases. However, a mutated form of the portion with the intestinal receptor for F18. The detection of the column of the intestinal receptor for F18. The detection of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polymorphic markers in the method disclosed enables the detection and treatment of E. coli-related intestinal diseases in swine, where there has been no success using antibiotics due to unsuccessful prophylaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        217 GGCATGTTCACGATCAATTCCATTGGCCGGCTGGGGAACCAGATGGGGGGAATACGCCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    397 ATCCCATGGCAGAATTACCATCTCAACGACTGGATGGAGGAGCGTTACCGCCACATTCCG
                                                                                                                                                                                                                                                                                    A method has been developed for the identification of swine that are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5e-108;
                               (BIOT-) BIOTECHNOLOGY RES & DEV CORP.
(SWTE-) SWISS FEDERAL INST TECHNOLOGY ZURICH.
(USDA ) US SEC OF AGRIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 423.8; D
Pred. No. 5e-10
0; Mismatches
                                                                                                                                                                                                                                                   Claim 6; Fig 1; 35pp; English
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69.6%;
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97US-0047181
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                                                                                            Vogeli P;
                                                                                                                         WPI; 1999-059746/05.
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Best Local Similarity
                                                                                                                                          P-PSDB; AAW30630
                                                                                            Bosworth BT,
 20-MAY-1997;
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                            CGGGGTTACCTGGAAAAGGCCCTGGATATGTTCCGGGCACGCTATTCATCTCCAGTGTTC
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GTGCGCCGAGGGGACTATGTGCATGTCATGCCTAATGTGTGGGAAGGGCCTGGTGGCTGAC
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P-PSDB; AAY79302

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This is the nuclectide sequence of the pig FUTI gene encoding alpha-1-2 fucosyltransferase (see AAY9302). A polymorphism at position 307 of the conding region is associated with susceptibility to FIB Escherichia coli colonization; pigs homozygous for adenine at position 307 are resistant to colonization, while heterozygous canimals and animals homozygous for quantine at position 307 are resistant to colonization. A claimed method for improving weight usceptible to colonization. A claimed method for improving weight resistant to E. coli colonization and feeding these animals high levels of plant-based protein concentrate. A claimed method for preventing FIB E. coli colonization in swine, especially swine that are genetically susceptible to FIB E. coli colonization, involves replacing some or all of the plant-based proteins in the diet with are genetically succeptible to FIB E. coli colonization, involves replacing some or all of the plant-based proteins in the diet with useful for developing drugs to treat swine that have E. coli associated disease. The polymorphism to the that have E. coli associated disease. The polymorphism can be detected using
                                   Improving weight gain in swine using swine genetically resistant Escherichia coli and feeding swine high levels of plant based protein
                                                                                                               Disclosure; Fig 1; 33pp; English.
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Matches 591; Conserv
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                                                   36.9%; Score 423.8; DB 21; Length 1269; 69.6%; Pred. No. 5e-108;
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Sequence 1269 BP; 219 A; 413 C; 362 G; 275 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents the swine alpha (1,2) fucosyltransferase (FUTI) gene. A FUTI gene in which there is a base other than adenine at position 307, may be used for improving weight gain in swine that are genetically susceptible to FIB Escherichia coii. The weight gain may be activated by feeding a diet of at least 40% animal based proteins. The feeding method is used to control FIB E. coli associated intestinal disease in swine.
                                                                                                                          CAGTGCAACCACATCATGACTATTGGGACCTTTGGGATTTGGGCTGCCTACCTGGCA
                                                                              GGTGGTGATACCATCTACTTAGCCAACTACACCCTTCCGGATTCTCCGGTTCCTCAAAGTC
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                                                                                                                                                                                                                                                                                                                                                Gene; pig; swine, alpha (1,2) fucosyltransferase; FUT1; weight gain;
F18; Escherichia coli; ss.
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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                AGCCTCCCGGTGTTACACACGGCCAAAAAGATCCCATGGCAGAATTACCATCTC
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APPLICANT: BTIC H. Holmes et al.
APPLICANT: ETIC H. Holmes et al.
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE
TITLE OF INVENTION: GAL-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 8511-029
CURRENT APPLICATION NUMBER: US/09/298,886
CURRENT APPLICATION NUMBER: US/09/298,886
SURRENT FILING DATE: 1999-04-26
SUFTWARE: PATCHIN VET. 2.0
SUFTWARE: PATCHIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/09298886 Patent No. 6329170
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                                                                                                    93.0%; Score 1068; DB 4; I
100.0%; Pred. No. 1.7e-301;
iive 0; Mismatches 0;
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                                                                                                                   Best Local Similarity 100.
Matches 1068; Conservative
                                                            ; LOCATION: (1)..(1062) US-09-298-886-9
LENGTH: 1068
TYPE: DNA
ORGANISM: Rattus n
FEATURE:
                                                    NAME/KEY: CDS
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2-ALHA-L-FUCOSYLITRANSFERASES, DNA SEQUENCES ENCODING
SAME, METHOD FOR PRODUCING THE SAME AND A METHOD OF
GENOTYPING A PERSON
    447 TACCCCTGCTCCTGGACCTTCTACCACCACCTGCGCACCGAGATCCTCCGGGAGTTCACC
                                                   ACCCTICCGGATTCTCCGTTCCTCAAGTCTTTAAGCCAGAGGCAGCCTTCCTACCGAA
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                                 CTGCATGACCACGTGCGGGAGGCCCAGGCCTTCCTGCGTGGTCTGCGGGTGAATGGG
                                                                                             AGCCAGCCGAGTACTTTGTGGGTGTCCATGTGCGCCGAGGGGACTATGTGCATGTCATG
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P. 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
ARLINGTON
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SOFTWARE: PatentIn Release #1.0, Version #1.
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28-PEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/08395800A Patent No. 5807732 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: LOWE, JOHN B
APPLICANT: LENNON, GREGORY
APPLICANT: ROUGUIER, SYLVIE
APPLICANT: GLORGI, DOMINIQUE
APPLICANT: KELLY, ROBERT J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (703) 413-3000
(703) 413-2220
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FILING DATE: 28-FEE
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US-08-395-800A-7
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APPLICANT: SANDELLAN G.
APPLICANT: SANDELLAN C. F.
TITLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
TITLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
TILE REPERBNCE: 30562.50800
CURRENT APPLICATION NUMBER: US/09/254,077A
CURRENT FILING DATE: 1997-06-11
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: PC 1823
PRIOR APPLICATION NUMBER: PO 1823
NUMBER OF SEQ ID NOS: 12
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                                                                                                                            Length 1043;
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Pred. No. 5.5e-174;
); Mismatches 203;
                                                                                                                                                                                                             Sequence 5, Application US/09254077A Patent No. 6399758
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76.9%;
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Best Local Similarity 76.9
Matches 814; Conservative
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                                                                                                                                                                                                                                                GENERAL INFORMATION:
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US-09-254-077A-5
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849 CAAGGACTICGCGCTGCTCACCCAGTGCAACCACCATCATGACTATTGGGACCTTTGG 908
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IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-220
TELEX: 24855 OPAT UR
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
ILNOGTH: 1144 base pairs
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1118 TTTCTCT 1126
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STRANDEDNESS: double
TOPOLOGY: linear
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Pred. No. 4.5e-169;
0; Mismatches 242;
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2115 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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74.78;
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US-08-395-800A-7
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APPLICANT: LOWE, JOHN B
APPLICANT: LOWE, GREGORY
APPLICANT: LENNON, GREGORY
APPLICANT: ROUGUIER, SYLVIE
APPLICANT: ROUGUIER, SYLVIE
APPLICANT: RELLY, ROBERT J
TITLE OF INVENTION: GDP-L-FUCOSE: BETA-D-GALACTOSIDE
TITLE OF INVENTION: 2-ALPHA-L-FUCOSYLTRANSPERASES, DNA SEQUENCES ENCODING THE TITLE OF INVENTION: SAME, METHOD FOR PRODUCING THE SAME AND A METHOD OF TITLE OF INVENTION: GROOTYPING A PERSON
NUMBER OF SEQUENCES: .22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                1029 CAICCCEGCCGAECTGTCCCCACFCCTFAAGGCAFTAACACCAGCCTGFCCTCGGTCCCA 1088
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                                                                    GATTIGGGCIGCCTACCIGGCAGGIGGIGATACCATCTACTTAGCCAACTACACCCTTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: U$/08/395,800A FILING DATE: 28-FEB-1995 CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Matches 642; Conserv
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591; Conservative
                                                                          ; OTHER INFORMATION: FUT1
US-09-151-592-1
                                                        LOCATION: (9)..(1103) FEATURE:
                                                                                                                   Similarity
      LENGTH: 1269
TYPE: DNA
ORGANISM: Swine
                                               NAME/KEY: CDS
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         CTGCGGGGCATGTTCACGATCAATTCCATTGGCCGGCTGGGGAACCAGATGGGCGAATAC
                  CGGGAGGACCTGTTCACTATCAACTCCAAGGGCCGCCTGGGGGAACCAGATGGGCGAGTAC
                                                          CTCCGCCAGGAGATCCTCCAGGAGTTCACCCTGCACGACCACGTGCGCGGAGGAGGCCCAG
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                                              GCCACACTCTTTGCACTGGCCAGGATGAACGGACGGCTTGCGTTCATCCCCGCATCCATG
                                                                                                       CACAGCAGGGTGGCCCCCCATCTTCAGAATCACCCTGCCGGTGCTGCACAGCGCCACGGCC
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GENERAL INFORMATION:

APPLICANT: BOSWOTTh, Brad

APPLICANT: Ridparth, Julia

APPLICANT: Wiseman, Barry

TITLE OF INVENTION: INTERACTIONS BETWEEN GENOTYPE AND DIET IN SWINE THAT

TITLE OF INVENTION: PREVENT E. COLI ASSOCIATED INTESTINAL DISBASE

FILE REFERENCE: 21419-90119
CURRENT APPLICATION WUMBER: US/09/151,592
CURRENT FILING DATE: 1999-09-18
NUMBER OF SEO ID NOS: 4
SOFTWARE: Patentin Ver. 2.0

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                                          Gaps
                                        9
Length 1269;
                                          Indels
  DB 4;
                                        252;
Score 423.8; DB 4;
Pred. No. 7.9e-114;
                                        0; Mismatches
  36.9%;
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                                                                                                                                                                                                                                                                              Length 1155;
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                                                                                                                                                                                                                                                                              Query Match 35.5%; Score 408.2; DB 1;
Best Local Similarity 68.7%; Pred. No. 2.6e-109;
Matches 579; Conservative 0; Mismatches 258;
                                                            Journal of Biological Chemistry
                                                                                                                                                                                                                      RELEVANT RESIDUES IN SEQ ID NO:
                    V.P. Rajan, et al.
PUBLICATION INFORMATION:
                                                                                                                    11158 - 11167
                                                                                                                                                                            FILING DATE:
PUBLICATION DATE:
                                                                                                                                                            DOCUMENT NUMBER:
                                                                                                                                     1989
                    AUTHORS:
TITLE:
                                                          JOURNAL:
VOLUME:
                                                                                                                                                                                                                                         US-08-208-889A-1
                                                                                                                    PAGES:
DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDENTIFICATION METHOD: DNA sequencing and restriction analysis
OTHER INFORMATION: The encoded product of nucleotide SEO ID NO:
OTHER INFORMATION: 1: is the enzyme, GDP-L-fuccose -D-galactoside 2-alpha-fucosy
OTHER INFORMATION: which has the amin ozid sequence described in SEO. ID NO:1:
OTHER INFORMATION: is responsible for the synthesis of 2'-fucosyllactose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: Cloned cDNA representing the product of a MOLECULE TYPE: human genomic DNA segment DESCRIPTION: GDP-L-fucose- -D-galactoside 2-alpha-fucosyl-transferase
                                                                                                                                                        APPLICANT: Prieto, P., Smith, D., Cummings, R., Kopchick, J., Mukerji, APPLICANT: Moremen, K., Pierce, J.
IITLE OF INVENTION: Transgenic Production of Oligosaccharides and TITLE OF INVENTION: Glycoconjugates
NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           intire amino acid sequence provided. Human Epidermal Carcinoma Cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diskette, 3.5 inch, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA: No. 5750176 applicable TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MS-DOS Version 6.21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: MordPerfect Version 6.0a CURREMY APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/208,889A FILING DATE: 09-MAR-1994
                                                                                                                                                                                                                                                                          ADDRESSE: Donald O. Nickey
ADDRESSE: ROSS Products Division
ADDRESSE: Abbott Laboratories
STREET: 625 Cleveland Avenue
                                                                                                                                                                                                                                                                                                                                                                                               United States of America
                                                                                             Sequence 1, Application US/08208899A Patent No. 5750176 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPAN: (614) 624-7080
TELEFAX: (614) 624-3074
TELEX: 0. 5750176e
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1155 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 43215
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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1083 CICCAGAIG 1091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
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POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 09 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                             Columbus
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TISSUE TYPE:
CELL TYPE:
CELL LINE:
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                                                                          US-08-208-889A-1
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                                                                                                                                                                                                                                                                                                                                                                          STATE:
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IDENTIFICATION METHOD: DNA sequencing and restriction analysis
OTHER INPORMATION: The encoded product of nucleotide SEQ ID NO:
OTHER INFORMATION: 1: is the enzyme, GDP-L-fucose--D-galactoside 2-alpha-fuc
OTHER INFORMATION: which has the amino acid sequence described in SEQ. ID NO:
OTHER INFORMATION: is responsible for the synthesis of 2'-fucosyllactose.
PUBLICATION INFORMATION:
AUTHORS: V.P. Rajan, et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 GCCATGTTCACGATCAATTCCATTGGCCGGCTGGGGAACCAGATGGGCGAATACGCCACA 275
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                                                                                                                                                                                                                                                       Journal of Biological Chemistry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                           PAGES: 11158 - 11167
DATE: 1989
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ISSUE:
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TITLE:
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                                                                                                                                                                                                                                                                                                                                                  Cummings, R., Kopchick, J., Mukerji, P.,
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MMEDIATE SOURCE: Human Epidermal Carcinoma Cell line
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS Version 6.21 SOFTWARE: WordPerfect Version 6.0a CUTRENT APPLICATION DATA: APPLICATION NUMBER: US/08/433,271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Donald O. Nickey
ROSS Products Division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             United States of America
                                                                                                                                                                                                                                                                                                                                 APPLICANT: Prieto, P., Smith, D., CAPPLICANT: Moremen, K., Pierce, J. TITLE OF INVENTION: Humanized Milk NUMBER OF SEQUENCES: I CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,122
FILING DATE: 09-MAR-1994
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                                                                                                                                                                                                                                                   Sequence 1, Application US/08433271
Patent No. 5891698
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CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
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TELEFAX: (614) 624-3074
TELEX: No. 5891698-
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 base pairs
TYPE: Nucleic acid
STRANDENNESS: Single
TOPOLOGY: UDKNOWN
WOLECULE TYPE: Cloned CDNA rep
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DEVELOPMENTAL STAGE:
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                                                                                                          GGACACTITIGTGCGCTTCACGGGATACCCGTGCTCCTGGACCTTCTACCACCACCTGCGC
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APPLICANT: LENNON, GREGORY
APPLICANT: ROUGUIER, SYLVIE
APPLICANT: GTORGI, DOMINIQUE
APPLICANT: KELLY, ROBERT J
TITLE OF INVENTION: GED-L-FUCOS
TITLE OF INVENTION: 3-ALPHA-L-F
TITLE OF INVENTION: SAME, METHO
TITLE OF INVENTION: GED-TPHA-L-F
TITLE OF INVENTION: GENOTYPING
NUMBER OF SEQUENCES: 22
CORRESPONDENCE: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 5807732
GENERAL INFORMATION:
APPLICANT: LOWE, C
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                                                                                                                                                                                                                                                                                                           Oligosaccharide Structures on Glycoproteins, Glycolipids, or as Free Molecules, and For the Isolation of Cloned Genetic Sequences That Determine These Structur
                                        TTTAAGCCAGAGGCAGCCTTCCTACCCGAATGGGTGGGCATCCCTGCCGATCTGTCCCCA 1050
   992 GGGGGAGACACTGTCTACCTGGCCAACTTCACCCTGCCAGACTCTGAGTTCCTGAAGATC 1051
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                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                       SSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADI.
SSEE: P.C.
P. Defferson Davis Highway, Suite 400
Arlington
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Pred, No. 2.1e-108;
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NAME: Lavalleye Ph.D., Jean-Paul
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-021-55 PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 10:
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FILING DATE: 19910214
CLASSIFICATION: 435
                                                                                                                                                                                                                                        Sequence 10, Application PC/TUS9100899 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
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577; Conservative
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CORRESPONDENCE ADDRESS
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                              CTC 1053
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PCT-US91-00899-10
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CITY: A
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                                      991
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Best Local
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1053 TITAAGCCGAGGCGCCTTCCIGCCCGAGTGGGGGGATTAATGCAGACTIGTCTCCA 1112
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     931 GGTGGTGATACCATCTACCTAGCCAACTACCCCTTCCGGATTCTCCGGTTCTCAAAGTC
                                                                                                                                                                                                                                                                                                                             APPLICANT: Sandrin, Mauro S.
APPLICANT: Fodor, William L.
APPLICANT: Rother, Russell P.
APPLICANT: Squinto, Stephen P.
APPLICANT: McKenzie, Ian F. C.
TITLE OF INVENTION: Methods for Reducing
TITLE OF INVENTION: Myperacute Rejection of Xenografts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS 6.2
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07554
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MOLECULE TYPE: CDNA to mRNA
DESCRIPTION: Human H-transferase
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                             Sequence 3, Application PC/TUS9507554 GENERAL INFORMATION:
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NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
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MEDIUM TYPE: 3.5 inch, 750
COMPUTER: Dell 486/50
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ADDRESSEE: Maurice M. Klee
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APPLICATION NUMBER: 08/260
FILING DATE: June 15, 1994
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APPLICATION NUMBER: 08/278
FILING DATE: July 21, 1994
CLASSIFICATION:
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TELEFAX: (203) 254-1101
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1951 Burr Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1174 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
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Ernst, L.K.
Nair, R.P.
Lowe, J.B.
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CITY: Fairfield
STATE: Connection
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AUTHORS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCTTTGCACTGGCCAGGATGAACGGACGGCTTGCGTTCATCCCCGCATCCATGCACAAC 336
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                                                                                                                                                                                                                                                                                                                                                                                          Length 1136;
                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 260; Indels
        MEDTOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/395,800A
FILING DATE: 28-FEB.1995
CLASSIFICATION: 435
TELEPOMMUNICATION: 1875
TELEPOMMUNICATION: 1730
TELEPAX: (703) 413-220
TELEPAX: 24885-OPAT UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                      Score 405; DB 1; I
Pred. No. 2.2e-108;
                                                                                                                                                                                                                                                                                                                                                                                      35.2%;
                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 68.4 Matches 577; Conservative
COMPUTER READABLE FORM:
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39..1133
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                                                                                                                                                                                                                                                                                                                        NAME/KEY:
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US-08-395-800A-9
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FEATURE:
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us-10-040-863-7.rni

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GDP-L-FUCOSE: BETA-D-GALACTOSIDE
2-ALPHA-L-FUCOSYLTRANSFERASES, DNA SEQUENCES ENCODING
SAME, METHOD FOR PRODUCING THE SAME AND A METHOD OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTE: TBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/395,800A
FILING DATE: 28-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 405; DB 1; I
Pred. No. 2.3e-108;
0; Mismatches 260;
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                                                                                                  Sequence 5, Application US/08395800A Patent No. 5807732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 413-220
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                            APPLICANT: ROUQUIER, SYLVIE
APPLICANT: GIORGI, DOMINIQUE
APPLICANT: KELLY, ROBERT J
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ilarity 68.4%;
Conservative
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                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
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TITLE OF INVENTION:
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les 577; Conserv
                                                                                                                              GENERAL INFORMATION: APPLICANT: LOWE,
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US-08-395-800A-5
                                                                 RESULT 12
US-08-395-800A-5
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                                                                                                                                                                                             Score 405; DB 5; )
Pred. No. 2.3e-108;
0; Mismatches 260;
Molecular cloning, sequence, and expression of a human GDP-L-fucose:
-1-galactoside 2-alpha.L-
fucosyltransferase cDNA that can form the H blood group antigen.
L: Proceedings of the National
L: Academy of Sciences, USA
                                                                                                                                                                                             35.2%;
68.4%;
                                                                                                                                                                                                            Local Similarity 68.4 tes 577; Conservative
                                                                                                                             6674-6678
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JOURNAL:
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                                                                                                               VOLUME:
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                                                                                                                                                                                                                           Length 2268;
                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                      Score 405; DB 4; 1
Pred. No. 3.1e-108;
); Mismatches 260;
DIAMOND=1A
       TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2268 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                      . 0
                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                    Query Match 35.2%;
Best Local Similarity 68.4%;
Matches 577; Conservative
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                    ; MOLECULE TY!
US-08-675-773B-4
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                         GTGCGCCGAGGGGACTATGTGCATGTCATGCCTAATGTGTGGAAGGGCGTGGTGGTGAC
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                                                                   CTGCGTGGTCTGCGGGTG-----AATGGGAGCCAGCCGAGTACTTTTGTGGGTGTCCAT
                                                                                              CIGGGTCAGCTCCGCCTCGGCCGCACAGGGACCGCCCGCGCACCTTTGTCGGCGTCAC
                                                                                                                                                                    GTGCGCCGTGGGGACTATCTGCAGGTTATGCCTCAGCCTGGAAGGGTGTGGTGGGGGGAC
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TOWNER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3: BROWDY AND NEIMARK, P.L.L.C.
419 SEVENTH STREET, N.W., SUITE 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DAILS
APPLICATION NUMBER: US/08/675,773B
FILING DAIE: 03-JUL-1996
CLASSIFICATION: 800
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: LOGAN, JOHN S
APPLICANT: BYRNE, GUERARD W
APPLICANT: SHARMA, AJAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,(
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                ACGCCGTGCCGGGAGCTGCAGCTTCACGACTGCACGCGGAGGAGGAGCTACGCGGACTTGAGA
                                                                                                                GGACACTITGIGGGCTTCACGGGATACCCGTGCTCCTGGACCTTCTACCACCACCTGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: LOGAN, JOHN S
APPLICANT: BYRE, GUERAED W
APPLICANT: SHRRA, AJAY
TILLE OF INVENTION: METHOD OF
TITLE OF INVENTION: FOR XENOTE
NUMBER OF SEQUENCES: 42
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MEDIUM TYPE: Floppy disk
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US-08-675-773B-3
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                                                                                                                                                                                                           Gastro-Intestinal
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/273,411
                                                                                                                                                                                                                                                                                          1100 Peachtree Street, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                         for
                                                                                                                                                      GENERAL INFORMATION:
APPLICANI: Falk, Per
APPLICANI: Gordon, Jeffrey I.
TILLE OF INVENTION: Animal Model for TITLE OF INVENTION: Disease
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sci.
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                                                                                                                       Sequence 2, Application US/08273411
Patent No. 5625124
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0
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NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: WUT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 815-6508
TELEFAX: (404) 815-6555
INFORMATION FOR SEQ. ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Nat'l Acad.
                                                                                                                                                                                                                                                                            Patrea L. Pabst
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68.4%;
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LOCATION: 104..1201
OUTHER INFORMATION: /oote-
PUBLICATION INFORMATION:
AUTHORS: Larsen, et al.
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CLASSIFICATION: 435
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       CTC 1053
                            |||
CTC 1591
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                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-273-411-2
                                                                                       RESULT 14
US-08-273-411-2
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STATE:
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Best Local S
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crc 3135
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Pred. No. 3.9e-108;
0; Mismatches 260; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,773B
FILING DATE: 03-VUL-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, INFR P.
                                                                                                                                                     DIAMOND=1A
                                                                                                                                  NAME: COOPEA, 1928 28,005
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: DIAM
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3791 base pairs
                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-675-7738-3
                                                                                                                                                                                                                                                                                                                                                  Query Match 35.2%;
Best Local Similarity 68.4%;
Matches 577; Conservative
                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
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May 26, 2003, 11:58:37 ; Search time 176.211 Seconds (without alignments) 861C.191 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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	Description	Sequence 7, Appli	Sequence 7, Appli	Sequence 9, Appli	Sequence 9, Appli	Sequence 1, Appli	Sequence 45, Appl	Sequence 1621, Ap	Sequence 234, App	Sequence 3, Appli	Sequence 12, Appl	Sequence 12, Appl	Sequence 9, Appli	-	29,		23,	Sequence 26, Appl	23,	Sequence 26, Appl
SUMMARIES	ΔΙ	US-09-999-672-7	US-10-040-863-7	US-09-999-672-9	US-10-040-863-9	US-09-051-034A-1	US-09-954-456-45	US-09-954-456-1621	US-09-969-347-234	US-09-051-034A-3	US-09-844-268-12	US-09-844-705-12	US-10-105-963-9	US-09-863-475A-5	US-09-999-672-29	US-10-040-863-29	US-09-999-672-23	US-09-999-672-26	US-10-040-863-23	US-10-040-863-26
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	% Query Match Length DB	1149	1149	1068	1068	1043	3088	3088	3088	1098	1269	1269	3373	8174	100	100	100	100	100	100
	% Query Match I	100.0	100.0	93.0	93.0	54.8	53.3	53,3	53.3	36.9	36.9	36.9	35.2	35.2	6,3	6.3	6.2	6.2	6.2	6.2
	Score	1149	1149	1068	1068	630.2	612.6	612.6	612.6	423.8	423.8	423.8	405	405	72.8	72.8	71.2	71.2	71.2	71.2
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Sequence 20, Appl Sequence 14, Appl Sequence 17, Appl Sequence 17, Appl Sequence 15, Appl Sequence 15, Appl Sequence 27, Appl Sequence 27, Appl Sequence 16, Appl Sequence 16, Appl Sequence 113, Appl Sequence 28, Appl Sequence 29, Appl Sequence 29, Appl Sequence 21, Appl Sequence 312, App	
US-09-999-672-20 US-09-999-672-14 US-09-999-672-14 US-09-999-672-14 US-10-040-863-14 US-10-040-863-14 US-10-040-863-15 US-09-999-672-15 US-09-999-672-27 US-09-999-672-27 US-09-999-672-16 US-09-999-672-16 US-09-999-672-16 US-09-999-672-18 US-09-883-28 US-09-883-28 US-09-883-28 US-09-883-28 US-09-883-28 US-09-883-28 US-09-883-28 US-09-883-28 US-09-999-672-28 US-10-040-863-28 US-09-999-672-28 US-10-040-863-28 US-10-040-863-28 US-09-999-672-19 US-10-040-863-28 US-10-040-863-28 US-10-040-863-28 US-10-040-863-28 US-10-040-863-28 US-10-040-863-28 US-10-040-863-28 US-10-040-863-19	
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ALIGNMENTS

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121 AAGGAATTACCGATGACGACTCAAATGTCCTCGGGAAACACAGAAAGCCCAGAGATGCGA 180
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                                                                         APPLICANT: Eric H. Holmes et al.

TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE
TITLE OF INVENTION: MALL-SPECIFIC ALPHAI-2 FUCOSYLIRANSFERASE AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: 8511-029
CORRENT APPLICATION NUMBER: US/09/999,672
CORRENT FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: US/09/298,886
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN VOIN S: 29
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100.0%; Pred. No. 0;
Live 0; Mismatches
                          Sequence 7, Application US/0999672 Patent No. US20020127655A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                          ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 1149; Conservative
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US-09-999-672-7
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RESULT 1
US-09-999-672-7
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                                                                                                                                                    AACGACTGGATGGAGGAGCGTTACCGCCACATTCCGGGACACTTTGTGCGCTTCACGGGA
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                             GGCCGGCTGGGGAACCAGATGGGCGAATACGCCACACTCTTTGCACTGGCCAGGATGAAC
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APPLICANT: Eric H. Holmes et al.

TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE
TITLE OF INVENTION: GAL-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 8511-029
COURRENT APPLICATION NUMBER: US/10/040,863
CURRENT FILING DATE: 1999-04-23
NUMBER OF SEQ ID NGS: 29
SOFIWARE: PATENTIN VOS: 29
SOFIWARE: PATENTIN VOS: 29
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                                                                                                                                                                 TYPE: DNA ORGANISM: Rattus norvegicus
                                                                                                                                                                                                              ; LOCATION: (1)..(1143)
US-10-040-863-7
                                                                                                                                                                                                  NAME/KEY: CDS
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Sequence 7, Application US/10040863 Patent No. US20020137165Al GENERAL INFORMATION:

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US-10-040-863-7

RESULT

181 GOCGAATAGGCCACACTCTTTGCACTGGCCAGGATGAACGGACGG	QY 742 CCRGTCTTCGTGGTTRACAGCAACGCTATCGCGGGAACATATATATCGTTCC 72 Db 661 CCAGTCTTCGTGGTTRACAACGCTAGGCCGGGGAACATATATTCC 72 CGAGGACACGTGGTTTCACACGCTAGGCCTGGTGCCGGGGAACATTATATTCCCTTCC 72 QY 802 CGAGGACGTGGTGTTCCCGGGCATGGTATTGGGGTCGCCAACCAA
	RESULT 3 RESULT 3 RESULT 3 Sequence 9, Application US/0999572 Sequence 10. 20200127655A1 Patent No. USCO00127655A1 REPLICANT: ELIA DE THE MORE Et al. TITLE OF INVENTION: UNCLED AND PROTEINS OF A RAT GANGLICSIDE TITLE OF INVENTION: HUEBER ET ACIDS AND PROTEINS OF A RAT GANGLICSIDE TITLE OF INVENTION: HERROF TOTAL ON 1999-072-9 SOUTHWER OF SEQ ID NOS: 29 SOUTH NOS: 29 SOUTHWER OF SEQ ID NOS: 29 SOUTHWER OF

1101

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181 CGGGACAGCGAGCAGCATGGAATGGAGGCTGCGGGGCATGTTCACGATCAATTCCATT 240
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922 TACCTGGCAGGTGGTGATACCATCTACTTAGCCAACTACACCCTTCCGGATTCTCCGGTTC
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APPLICANT: SANDRIN, MAURO SERGIO
TITLE OF INVENTION: IMPROVED NUCLEIC ACIDS ENCODING A CHIMERIC
TITLE OF INVENTION: GLYCOSYLTRANSFERASE
FILE REFERENCE: 30562.60SNO
CURRENT APPLICATION NUMBER: US/09/051,034A
CURRENT FILING DATE: 1998-03-31
PRIOR FILING DATE: 1997-09-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      60/024,279
                                                                                                                                                                                                                                                                            Sequence 1, Application US/09051034A Patent No. US20010055584A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: 60/024,
PRIOR FILING DATE: 1996-08-21
PRIOR APPLICATION NUMBER: 901402
PRIOR FILING DATE: 1996-08-02
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US-09-051-034A-1
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US-09-051-034A-1
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                                                                                                                                                                             93.0%; Score
100.0%; Pred. No. v.
... 0; Mismatches
PRIOR APPLICATION NUMBER: 09/298,886 PRIOR FILING DATE: 1999-04-23
                                                                                                   ÓRGANISM: Rattus norvegicus
                         NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
                                                                                                                                                                                                    Best Local Similarity 100.
Matches 1068; Conservative
                                                                                                                              NAME/KEY: CDS
; LOCATION: (1)..(1062)
US-10-040-863-9
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PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PATCHIN VERSION 3.0
SEQ ID NO 455
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GENERAL INFORMATION:
Fatent No. US20020115057Al
GENERAL INFORMATION:
FAPLICANT: Young, Paul
TITLE OF INVENTION: Sets
FILE REFRENCE: 682907-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
FRIOR APPLICATION NUMBER: US/60/23,617
FRIOR PAPLICATION NUMBER: US/60/234,052
FRIOR PAPLICATION NUMBER: US/60/234,923
FRIOR PAPLICATION NUMBER: US/60/234,923
FRIOR PAPLICATION NUMBER: US/60/235,134
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FRIOR PAPLICATION NUMBER: US/60/235,637
FRIOR PAPLICATION NUMBER: US/60/235,637
FRIOR APPLICATION NUMBER: US/60/235,638
FRIOR FILING DATE: 2000-09-26
FRIOR APPLICATION NUMBER: US/60/235,638
FRIOR FILING DATE: 2000-09-26
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180 CACTATATTCACGTTCAGCAGCGGCTAGCGAAAGCCCAGCCATGTGGGAGTTACCGGT 23 129 ACCGATGACGACTCAAATGTCCTCGGGAAACACAGAAAGCCCAGGGATGCGACGGAACAG 18	309 TGGTTCATCCCGCATCCATGCACAACGCTCTAGCGCCCATCTTCAGGATCAGCCTCCC 368 367 GITTLITTITTITTITTITTITTITTITTITTITTITTITT	489 CTCCTGGACCTTCTACCACCACGCCCAGAGATCCTGAAGGAGTTCACCCTGCATGA 54	669 GTGGAAGGCGTGACCGGGGTTACCTGGAAAAGGCCCTGGATATGTTCCC 747 GTGGAAGGGGTGGTGGCGGGGTTACCTGGAAAAGGCCCTGGATGTTCCC 75 AGCTATTCATCTCCGGCGATACCTACAGGAGGCCTGGTGCGGGG 75 AGCTATTCATCTTCGTGGTTACAGGAAGGCGTGGTGCCGGGG 76 TGGTAAGCTTCCAGTTTCGTGGTTACAGGAAGGCTGGTGCGGGGG 78 CATTAAGCTTCCAGGGGGGGTGTTCGCGGCAATGGCTGGTGGGGGGGG	1047 1029 1107 1089 1167 SULT 8
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	1029 CATCCTGCCGATCTGTCCCCACTCCTTAAGGCATTAACACCAGCCTGTCCTCGGTCCCA 108	Sequence 1621, Application US/09954456 Patent No. US20020115057A1 GENERAL INFORMATION: APPLICANT: Young, Paul TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand TITLE OF INVENTION: Sets TITLE OF INVENTION UNMER: US/09/954,456 CURRENT FILING DATE: 2001-09-18 PRIOR PLICATION NUMBER: US/60/233,617 PRIOR PLING DATE: 2000-09-18 PRIOR PLING DATE: 2000-09-18 PRIOR APPLICATION NUMBER: US/60/234,052	FILING DATE: 2000-09-20 APPLICATION NUMBER: US/60/234,92 APPLICATION NUMBER: US/60/234,92 APPLICATION NUMBER: US/60/235,13 FILING DATE: 2000-09-25 APPLICATION NUMBER: US/60/235,63 FILING DATE: 2000-99-26 APPLICATION NUMBER: US/60/235,63 FILING DATE: 2000-99-26 APPLICATION NUMBER: US/60/235,71 FILING DATE: 2000-09-27 APPLICATION NUMBER: US/60/235,84 FILING DATE: 2000-09-27 FILING DATE: 2000-09-27 APPLICATION NUMBER: US/60/235,86 APPLICATION NUMBER: US/60/235,86 APPLICATION NUMBER: US/60/235,86	% ORGANISM: Homo sapiens US-09-954-456-1621 Query Match Sa.3%; Score 612.6; DB 10; Length 3088; Best Local Similarity 73.8%; Pred. No. 1.5e-185; Matches 808; Conservative 0; Mismatches 254; Indels 33; Gaps 1; Qy 9 CGCCCAGGTTCCTTTCTCTCTGCGCCCACTTCTTTTTCTTTGCTTTCTGAGACTTC 68 Db 120 GGTCAGATCCTTTCCCTTTCCCATGGCCACTTCTTTTTTTT

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1047 CGACTCCCCTTTCCTCAAATCTTTAAGCCAGAGCAGCCTTCCTGCCGGAGTGGACAGG 1106
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                             CAAGGACTTCGCGCTGCTCACCCAGTGCAACCACCATCATGACTATTGGGACCTTTGG
       729 ACGCTATTCATCTCCAGTCTTCGTGGTTACAAGCAACGGTATGGCCTGGTGCCGGGAGAA
                                                                                CATIAATGCTTCCCGAGGAGACGTGGTGTTCGCGGGCAATGGTATTGAGGGCTCGCCAGC
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APPLICANT: MCKRAZIE, IAN FARQUHAR CAMPBELL
APPLICANT: MCKRAZIE, IAN ERROTOR
APPLICANT: BANDRIN, MAURO SERGIO
TITLE OF INVENTION: IMPROVED NUCLEIC ACIDS ENCODING A CHIMERIC
TITLE OF INVENTION: GLYCOSYLTRANSFERASE
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Pred. No. 2.6e-125;
0; Mismatches 252;
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CURRENT APPLICATION NUMBER: US/09/051,034A
CURRENT FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: PCT/AU97/00492
PRIOR PILING DATE: 1997-08-01
PRIOR PILING DATE: 1996-08-21
PRIOR PILING DATE: 1996-08-21
PRIOR PILING DATE: 1996-08-21
PRIOR APPLICATION NUMBER: P01402
PRIOR APPLICATION NUMBER: P01402
NUMBER OF SEO ID NOS: 14
SOFTWARE: PATENTIN VOICE: 121
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Best Local Similarity 69.6
Matches 591; Conservative
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US-09-051-034A-3
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Sequence 234, Application US/09969347

Batent No. US20020115085A1

Batent No. US20020115085A1

Batent No. US20020115085A1

BAPPLICANT: Boner, Reinhard

TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signaturing OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signaturing OF INVENTION: Sets

FILE REPERENCE: 689290-69

CURRENT APPLICATION NUMBER: US/09/969,347

CURRENT FILING DATE: 2000-10-02

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

NUMBER: OF SEQ ID NOS: 318
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Pred. No. 1.5e-185;
0; Mismatches 254; Indels 33;
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SEQ ID NO 234
LENGTH: 3088
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US-09-969-347-234
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TILLE OF INVENTION: METHODS AND COMPOSITIONS TO IDENTIFY SWINE GENETICALLY
TITLE OF INVENTION: RESISTANT TO FIR E. COLI ASSOCIATED DISEASES
FILE REFERENCE: 21419/90368
CURRENT APPLICATION NUMBER: US/09/844,268
CURRENT FILING DATE: 2001-04-27
                                                                                                                                                           CAGTGCAACCACACCATCATGACTATTGGGACCTTTGGGATTTGGGCTGCCTACCTGGCA
                                                                    GAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTACACACCCTCGG
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        ATCCCATGGCAGAATTACCATCTCAACGACTGGATGGAGGAGCGTTACCGCCACATTCCG
                            GCTCCTTGGCGGGGGCTGGAGCTTCACGACTGGGATGTCCGAGGATTATGCCCACTTAAAG
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PRIOR FILING DATE: 1999-11-19
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SOFTWARE: PatentIn Ver. 2.
SEQ ID NO 12
LENGTH: 1269
TYPE: DNA
ORGANISM: Porcine
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APPLICANT: BOSWORTH, BRAD
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                                                                                      217 GGCATGTTCACGATCAATTCCATTGGCCGGCTGGGGAACCAGATGGGCGAATACGCCACA
                                                                                                                                                                        CTCTTTGCACTGGCCAGGATGAACGGACGGCTTGCGTTCCATCCCCGCATGCACAAC
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Length 1269;
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  DB 10;
                                           0; Mismatches 252;
Score 423.8; DB 10
Pred. No. 2.8e-125;
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  36.9%;
69.6%;
                                             Conservative
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                      Similarity
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1083 CTCCAGATG 1091
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
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APPLICANT: VOGELL, PETER
TITLE OF INVENTION: METHODS AND COMPOSITIONS TO IDENTIFY SWINE GENETICALLY
TITLE OF INVENTION: RESISTANT TO FIG E. COLI ASSOCIATED DISEASES.

FILE REFERENCE: 21419/90368
CURRENT APPLICATION NUMBER: US/09/844,705
CURRENT FILING DATE: 2001-04-27
PRIOR PELLOR DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 13
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69.6%; Pred. No. 2.8e-125;
iive 0; Mismatches 252;
                                                                                                                                 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                  ; LOCATION: (9)..(1103)
US-09-844-705-12
                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                         TYPE: DNA ORGANISM: Porcine
                                                                                                                                                                                                                   NAME/KEY: CDS
                                                                                                                                                            LENGTH: 1269
                                                                                                                                                                                                                                                                                                       591;
                                                                                                                                              ID NO 12
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APPLICANT: Denning, Chris
APPLICANT: Denning, Chris
APPLICANT: Clark, A. John
APPLICANT: Clark, A. John
APPLICANT: Clark, A. John
TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Compatible for Human
TITLE OF INVENTION: Transplantation and a Carbohydrate Determinant Selection Syst
TITLE OF INVENTION: Recombination
TITLE OF INVENTION: 1002-03-21
NUMBER: PAPLICATION NUMBER: US 60/277,811
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin version 3.1
SEQ ID NO 9.
963 GGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGGTTCCTGAAGATC 1022
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                                                                 991 ITTAAGCCAGAGGCAGCCITCCTACCCGAATGGGTGGGCATCCCTGCCGATCTGTCCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/10105963
Publication No. US20030668818A1
GENERAL INFORMATION:
APPLICANT: Geron Corporation
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Best Local Similarity 68.4
Matches 577; Conservative
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                                                                                                                                                                                                          260;
                                                                                                                                                                    Score 405; DB 10;
Pred. No. 6.2e-119;
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                                                                                                                                                                    Score 405;
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ON
                                                                                                              SEQUENCE DESCRIPTION: SEQ ID
                                                          TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
         LENGTH: 8174 base pairs
                        TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                  35.2%;
68.4%;
                                                                                                                                                                                                        Conservative
                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL INFORMATION.
APPLICANT: LOWE, JOHN B.
TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
                                                                                                                                                                                                                                                                                                             1057
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                                                                                                                                                                                                                                                                                          GCCGGAGACACTGTCTACCTGGCCAACTTCACCCTGCCAGACTCTGAGTTC
                                                        CGGGGTTACCTGGAAAAGGCCCTGGAIATGTTCCGGGCACGCTATTCATCTCCAGTCTTC
                                                                                         AGCGCCTACCTCCGGCAGGCCATGGACTGGTTCCGGGCACGGCACGAAGCCCCCGTTTTC
                                                                                                                         GIGGITACAAGCAACGGIATGGCCTGGTGCCGGGAGAACATTAATGCTTCCCGAGGAGAC
                                                                                                                                                                                                GIGGIGITCGCGGCAATGGTATTGAGGGTCGCCAGCCAAGGACTTCGCGCTGCTCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Lavalleye, Jean-Paul M. P.
REGIESTRATION NUMBER: 31,451
REFERENCE/DOCKEY NUMBER: 2363-060-55
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/863,475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/914,281
FILING DATE: 20-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 24-May-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09863475A
Patent No. US20020102688A1
GENERAL INFORMATION:
APPLICANT: LOWE, JOHN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
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US-09-863-475A-5
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827 ATGGTATTGAGGGGTCGCCAGCCAAGGACTTCGCGCTGCTCACCCAGTGCAACCACCA 886
                 Sequence 29, Application US/0999672

Patent NO. US2002012012655A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TOTALE OF INVENTION:
TITLE APPLICATION NUMBER: US/09/999,672

CURRENT APPLICATION NUMBER: US/09/298,886

NUMBER OF SEQ ID NOS: 29
SEQ ID NOS: 29
SEQ ID NO 29
LENGTH: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Eric H. Holmes et al.
APPLICANT: Eric H. Holmes et al.
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE
TITLE OF INVENTION: GML-SPECIFIC ALPHAl-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENTION: THRREOF
FILE REFERENCE: 8511-029
CURRENT APPLICATION NUMBER: US/10/040,863
CURRENT PILING DATE: 2001-11-01
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATCHIN VET. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 6.3%; Score 72.8; DB 10; Length 100; 1 Similarity 83.0%; Pred. No. 2.4e-13; 83; Conservative 0; Mismatches 17; Indels 0
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US-10-040-863-29
Sequence 29, Application US/10040863
Patent No. US20020137165A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA; ORGANISM: Oryctolagus cuniculus US-09-999-672-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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US-09-999-672-29
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827 ATGGTATTGAGGGGTCGCCAGCCAAGGACTTCGCGCTGCTCACCCAGTGCAACCACCACAA 886 61 TCATGACCATCGGCACCTTTGGGATCTGGGCCCCTACCT 100 887 ICAIGACTAITGGGACCTITGGGAITTGGGCTGCCTACCT 926 Search completed: May 26, 2003, 15:19:53 Job time: 178.211 secs

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May 26, 2003, 10:09:53 ; Search time 1886.5 Seconds (without alignments) 9864.119 Million cell updates/sec
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1149
1 atggccagcgcccaggttcc......gaagagccttctgatgggaa 1149
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GenCore version 5.1.6 Copyright (c) 1993 ~ 2003 Compugen Ltd.
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                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	BB624949 BB624949	BO920588 AGENCOURT	BE266792 601190486	BM744084 K-EST0017	BM764661 K-EST0046	BM781532 K-EST0058
SUMMARIES	ID	BB624949	BQ920588	BE266792	BM744084	BM764661	BM781532
	DB	10	14	10	14	14	14
	Query Score Match Length DB II	656	1133	714	296	590	291
æ	Query Match	35.7	34.7	29.9	24.6	24.0	23.8
	Score	410	398.6	343.8	283	275.4	273.2
	Result No.	П	c 5	m	4	'n	9

888 171 172 170 190	719 6009- 859 BB844 101 2459- 117 2105- 117 CM4- 152 RC6- 120 RSTI:	28 28 28 28 28 28 28	74 CH23(89 1553; 528 bb57(127 BB85(127 CM0-1 337 CM0-1	BH342476 CH230-111 BM742943 K-ESTG015 AU100082 AU100082 AL709188 DKFZp686B BM974044 UL-CF-EC1 BG60050 326648 MA BM758349 K-ESTG037 BF418108 UI-R-CAO- AIG06683 M156f10.Y AA108903 M156f10.Y
A BM76478 AL046138 BM76475 BF71051 BB84954 7 BH27450 BM77335	0 BE2997 0 BB8488 2 BF1941 2 BE7564 0 AW8439 2 BF3580 2 BG1928 2 BG1928	0 AW34766 3 BJ09103 7 AZ28516 2 BF93032 3 BI53476 3 BJ04099 2 BF30402	7 BH34247 0 BE66758 0 BE01952 0 BB85012 0 AW91791 0 AW83883 3 BI35005	BH34247 BM74294 AUT00082 AL709188 BM97404 BM75834 BF41810 AI606683 AA108903
3.7 7.83 33.7 7.83 11.5 5.93 8.9 444 5.2 5.2 5.2 5.2 5.2 5.2 5.2 5.2 5.2 5.2	2. 4. 2. 4. 4. 6. 6. 6. 6. 6. 6. 6. 6. 6. 6. 6. 6. 6.	3.9 1.9 1.9 5.0 0.7 4.2 0.5 6.5 8.3 8.3	.3 .0 .0 .0 .0 .0 .0 .0 .0 .0 .0 .0 .0 .0	6.000000000000000000000000000000000000
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ALIGNMENTS

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/dlone="ImAGE:6497629"
/clone=lib="NNIH_MGC_101"
/tissue_type="epidermoid carcinoma, cell line"
/tas_host="bildow (phage resistant)"
/note="Organ: lung: Vector: pOTB7: Site_1: EcoR1; Site_2:
/note="Organ: lung: Vector: poTB7: Site_2: Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BQ920588 IIInear EST 20-AUG-2002 AGENCOURT_10016100 NIH_MGC_101 Homo sapiens cDNA clone IMAGE:6497629 5', mRNA sequence.
                    235 AAGGAATTAC---AGGCGGTTCAAATGTCCTCACCAAACGCGGCAAGAACAGACATG---
                                                                                    CGGGACAGCGAGCATGGGAATGGAGAGCTGCGGGGCATGTTCACGATCAATTCCATT
                                                                                                                                                -------CAGCAGAGTGCCAAGCTGCAGGGCATATTCACGATCAATTCCATC
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1133)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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High quality sequence stop: 440.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A., Aizawa,K., Pukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K., Arakawa,T.,
Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
Func. Genomics 2 pre, L72-186 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                           sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
Bmail: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.P. Shibata.Y. Hayatsu.N., Sugahara.Y., Shibata,K., Itoh
Carninci.P. Okazaki.Y. Hayatsu.N. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi.K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 ATGGCGAGTGCCCANNTACCTTTCTCTCTCTGGCCCACTTCCTCTTTTTTT 174
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Pred. No. 1.7e-102;
0; Mismatches 57; Indels 21; Gaps
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/clone="9030420L11"
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/dev_stage="adult"
/lab_host="DH10B"
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FEATURES

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/note="Organ: lung; Vector: porBS; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GG-ACGAGGG(5). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCCTGGACCTTCTACCACCACCACCAGCCCAGAGATCGTGAAGGACTTCACCCTGCATGA
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                                                                                                                                                                                                                                                                                      35;
                                                                                                                                                                                                                                                       DB 10; Length 714;
                                                                                                                                                                                                                                                      29.9%; Score 343.8; DB 10; Length llarity 73.2%; Pred. No. 3.9e-84; Conservative 0; Mismatches 147; Indels
                 /clone_lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DHIOB (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTGGAAGGGCGTGGTGGC 686
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                                                                                                                                                                                                                                                                                                                                  353 AGTICCTGCGGGCCTGCAGGTGAACGGGAGCCGGCCGGCCACCTTTGTAGGGGTCCATG
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                                                                                                                                                                                        CCTTCCTGCGTGCTCTGCGGGTGAATGGGAGCCAGCCGAGTACTTTTGTGGGGTGTCCATG
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                                                                                                                          333 CAACGCTCTAGCCCCCATCTTCAGGAT-CAGCCTCCCGGTGTTACACAGCGACACGCCCA
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                               Length 1133;
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                                                                                              Indels
                                                               DB 14;
                                                                                              Mismatches 114;
                                                             Score 398.6; DB 1/
Pred. No. 3.3e-99;
                 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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Library."
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80.6%;
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RESULT 3 BE266792

q 22

ACCESSION VERSION KEYWORDS

FEATURES

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21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
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/db_xref="taxon:9666"
/clone="s3sNu16s1-7-H02"
/clone=lib="$3sNu16s1"
/sex="F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: yongsung@mail.kribb.re.kr
Plate: 7 row: H column: 02
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Location/Qualifiers
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                                                                                                                                                                     1 (bases 1 to 596)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
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                                                                                                             Homo sapiens
Eukaryota; Metazca; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 CGCCCAGGITCCTITCICCTITCCTCTGGCCCACTICCTCATCTITGICTTCGTGACTTC
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                                                                                                                                                                                                                                                                                                                                                    52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-866-4470
Fax: +82-42-860-4409
                                                                                                                                                                                                                                                                                                                                              Korea Research Institute of Bioscience & Biotechnology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.6%; Score 283; DB 14; Length 596; llarity 71.7%; Pred. No. 2.5e-67; Conservative 0; Mismatches 125; Indels 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="Lymphoblast-like"
/cell_line="SNU-16"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S3SNU16-14-A06"
                                                                                                                                                                                                                                                                                                                                                                                                                            Email: yongsung@mail.kribb.re.kr
Plate: 14 row: A column: 06
High quality sequence stop: 596.
Location/Qualifiers
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/sex="F"
                      BM744084
BM744084.1 GI:19065413
                                                                                                                                                                                                                                                                                                   Contact: Kim YS
Genome Research Center
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1 (bases 1 to 590)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y.. Kim.M R
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                                                                                                                                                309 TECETICATCCCECATCCATECATECACACECTCTAGCECCCATCTTCAGGATCAGCCTCCC
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Korea Research Institute of Bioscience & Biotechnology
52 Eceun-dong Yuscong-qu, Daejeon 305-333, South Korea
Pel: +82-42-860-4409
Fax: +82-42-860-4409
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Query Match
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                                                 SOURCE
ECORI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method: The converted to a DNA strand by Okayama-Berg method: The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2.000 - 3.000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including TY promotor as 5 primer and N(dT)14 as 3 primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with library and isometry and its stranded cDNAs prepared from original
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 CACCATCATCCACCTCCAGCAGCAATAGTGAAGCTCCAACCCCTGTCAGAGAAGTT 128
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                                                                                                                                                                                                                                                                                                      liberary and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted CDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli ToploF' with electroporation method."
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71.2%;
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BM781532 591 bp mRNA linear EST 05-MAR-2002 K-EST0058109 53SNU16s1 Homo sapiens cDNA clone S3SNU16s1-19-B07 5',

mRNA sequence. BM781532

DEFINITION

BM781532

ACCESSION

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/note="Organ: Stomach; Vector: pT218RP1; Site_1: ECORI; Site_2: Not1: The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including ECOR is site by treatment of T4 RNA ligase and the first strand CDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60Mt. The cDNA vector was circularized with E. coli DNA ligase after digestion of ECORI which site is also included in vector. An RNA strand converted to a DNA strand by Osayama-Berg method. The obtained CDNA vectors were used for transformation of competent cells E. coli ToplOF' by electroporation method. The cDNA libraries constructed by this method are full-length enriched CDNA library. After analyzing and sequencing about 2,000 - 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original liberary and incubated with avidin-gel. After removing DNA-RNA hybrids Dy centrifuge, the subtracted CDNA interference of the removing DNA-RNA hybrids Dy centrified, the subtracted constructed by transformation of the
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                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 591)
                                                                                                                                                                                                                                                              Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.F
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Korea Research Institute of Bioscience & Biotechnology 52 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 19 row: B column: 07
High quality sequence stop: 591.
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/sex="F"
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BM781532.1 GI:19129764
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                                                                                                                   Homo sapiens
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Kim.N.S., Hahn,Y., Oh.J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Sim.Y.S.
21C Frontier Korean EST Project 2001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ACCGATGACGACTCAAATGTCCTCGGGAAACACAGAAAGCCCAGAGATGCGACGGGACAG
                                                                                                                                                                            TGCGTTCATCCCCGCATCCATGCACAACGCTCTAGCGCCCATCTTCAGGATCAGCCTCCC
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                                                                             191 GCAGATACCATGGCTAGCCTCAACATCAAAGGCACTGAGACCCATCC-
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/cell_line="SNU-16"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: yongsung@mail.kribb.re.kr
Plate: 4 row: D column: 03
High quality sequence stop: 587.
Locatton/Qualifiers
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/sex="F"
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Contact: Kim YS
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LOCUS

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adjusted to have about outs. The cura vector was circularized with site is also included in vector. An RNA strand converted to a DNA strand by Okayama berg method. The coharted to a DNA strand by Okayama berg method. The obtained cohar vectors were used for transformation of competent cells E. coli ToplOF' by electroporation method. The coha libraries constructed by this method are full-length enriched cDNA libraries of the cohart in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5 primer and N(dT)14 as 3 primer. PCR products were used as template for synthesis of products were used as template for synthesis of blotinylated single stranded RNA by in vitro transcription reaction. The Synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original libraries were constructed by transformation of the remaining DNA into competent cells E. coli ToplOF' with electroporation method."
                        /note="Organ: Stomach; Vector: pT218RP1; Site_1: ECORI; Site_2: NOTI: The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including ECOR I site by treatment of T4 RNA ligase and the first strand CDNA was synthesized from Oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The CDNA vector was
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Pred. No. 2.1e-64;
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lab_host="Top10F'"
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71.1%;
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Matches 391; Conservative
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/note="Organ; Stomach; Vector: pTz18Rp1; Site_1: ECORI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including ECOR I site by treatment of T4 RNA ligase and the first strand CNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coll DNA ligase after digestion of ECORI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coll ToplOF' by electroporation method. The CDNA libraries constructed by this method are
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Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, M.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and S.M., Y.S.

21C Frontier Korean EST Project 2001

Unpublished (2002)

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52 Ecoun-dong Yuscong-qu, Daejeon 305-333, South Korea

Fax: +82-42-860-4470

Fax: +82-42-860-4470
                                                                                                                                                                                                                                                975 TCCGITCCTCAAAGICITTAAGCCAGAGCAGCCTTCCTACCCGAATGGGTGGGCATCCC 1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BM764751 592 bp mRNA linear EST 04-MAR-2002
K-EST0046310 S3SNU16s1 Homo sapiens CDNA clone S3SNU16s1-5-H66 5',
                                                                    CTTCGCGCTGCTCACCCAGTGCAACCACACATCATGACTATTGGGACCTTTGGGATTTG 914
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                           299 CITCGCACTGCTCACAGTGCAACCACACCATCATCACCGTGGGCACCTTCGGGGTCTG
359 GGCGCGGTACCTCGCGGGGGGGACACTGTGTACCTGGCCCAACTC
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Plate: 5 row: H column: 06
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High quality sequence stop: 5
Location/Qualifiers
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                                                                                                              DKFZp434P0672_r1 434 (synonym: htes3) Homo sapiens cDNA clone

DKFZp434P0672_r1, mRNA sequence.

AL046138

BAL046138.2 GI:5936190
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: poustka@mpimg-berlin-dahlem.mpg.de
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2): Email S. Wiemann@dkfz- heidelberg.de,
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No s1 sequence available.
This clone (DKFZp434P0672) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY: Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 764)
Poustka, A., Klein, M., Mewes, H.W., Gassenhuber, J. and Wiemann, S. EST (boustka, et al.)
Unpublished (1999)
On Jul 9, 1999 this sequence version replaced gi:5434225.
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248 g 157 t 3 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department Lehrach
Max-Planck-Institute for Molecular Genetics
Inhestrasse 73, 14195 Berlin, Germany
Tel: +49-30-84131128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="434 (synonym: htes3)"
/tissue_lype="testis"
/dev_stago="adult"
/lab_lost="DH10B"
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/db_xref="taxon:9606"
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234 c 24
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73.6%;
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CCACGIGGGG 558
                                          CCACGIGCGG 587
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549
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SOURCE
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                                                                                                          RESULT 8
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/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/note="Westor: p773D-pac (Pharmacia) with a modified
/note="Westor: p773D-pac (Pharmacia) with a modified
polylinker; Site_I: Not I; Site_2: EcoRI; The MI-P-AYI
library is normalized library derived from the MI-P-AYO
library, ultimately derived from placenta tissue. For a
detailed description of the library from which this clone
was derived, please visit our web site at
http://pigest.genome.lastate.edu/. The procedure used to
create this library has been previously described (Bonaldo
, Lennon and Soares, Genome Research 6: 791-806, 1996)
                                                                                                                                                                                                                                                                                                                          Email: cktuggle@iastate.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the Notl site and the oligo-dT track served to verify it as a clone from the normalized placenta library CDNA Library Preparation: M.B. Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab, University of Iowa Clone distribution: clones will be available through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1011 CCTACCCGAATGGGIGGGCATCCCTGCCGATCTGTCCCCACTCCTTAAGGCCATTAACACC 1070
                                                                                    facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 711 CCTGGATATGTTCCGGGCACGCTATTCATCTCCAGTCTTCGTGGTTACAAGCAACGGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCCAACTACACCTTCCGGATTCTCCGTTCCTCAAAGICTTTAAGCCAGAGGCAGCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            281 GGCCAATTACACGCTCCCGGACTCTCCTTCCTCAAACTCHTTAAGCCCGAGGCAGCCTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             771 GOCCTGGTGCCGGGAGACATTAATGCTTCCCGAGGAGACGTGGTGTTCGCGGGCAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              831 TATIGAGGGTCGCCAGCCAAGGACTICGCGCTGCTCACCCAGTGCAACCACCATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACTATTGGGACCTTTGGGATTTGGGCTGCCTACCTGGCAGGTGGTGATACCATCTACTT
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                                                                                                                                                                                                          Molecular Genetics Laboratory, Department of Animal Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 521;
               Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
1 (bases 1 to 521)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                       9
                                                                                    Normalization and subtraction: two approaches
                                                                                                                                                                                                                                 Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 247; DB 12;
Pred. No. 2.2e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="MI-P-AX1-nre-a-12-0-UI"
/clone_lib="MI-P-AX1"
                                                               Lennon, G. and Soares, M.B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Research Genetics (www.resgen.com)
                                                                                                                                     Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Sus scrofa"
/strain="crossbreed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAG_TISSUE=placenta
TAG_SEQ=ATTGG"
119 c 170 q
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                                                                                                                                                                                     Contact: Tuggle CK
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Best Local Similarity 79.1
Matches 306; Conservative
                                                                                                                                                                                                                                                                               Tel: 5152944252
Fax: 5152942401
                                                             Bonaldo, M.F.,
                                                                                                                discovery
                                                                                                                                                            97044477
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                                      REFERENCE
                                                               AUTHORS
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full-length enriched CDNA library. After analyzing and sequencing about 2,000 - 3,000 colonies in original CDNA library, the abundant CDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single strandad RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original liberary and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli ToplOF' with electroporation method.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACCATCATCCACCTCCAGCAGCGAATAGTGAAGCTCCAACCCCTGTCAGAGAAGTT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTGTTACACAGGGACACGGCCAAAAAGATCCCAIGGCAGAATTACCATCTCAACGACTG 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 ACCGATGACGACTCAAATGTCCTCGGGAAACACAGAAAGCCCAGAGATGCGACGGGACAG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAIGGAGGAGCGITACCGCCACATICC-GGGACACITIGIGCGCTICACGGGATACCCGT 487
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Sus scrofa
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309 TGCGTTCATCCCCGCATCCATGCACAACGCTCTAGCGCCCATCTTCAGGATCAGCCTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTCCTGGACCTTCTACCACCACCTGCGCCCCAGAGATCCTGAAGGAGTTCACCCTGCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGCCCAGGITCCTTTCTCCTTTCCTCTGGCCCACTTCCTCATCTTTGTCTTCGTGACTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191 GCAGATACCAGTGCTAGCCTCAACATCAAAGGCACTGGGACCCA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34;
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 265.4; DB 1. Pred. No. 1.9e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                              23.1%;
71.2%;
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CH230-22L10.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone BH274506
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                                                                                                                                                                                                                                                                                                                                                    88 ATGGCGAGTGCCCAGGTACCTTTCTCCTTTTCCTCTGGCCCACTTCCTCATCTTTGTCTTT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGGGACAGCGAGCAGCATGGGAATGGAGAGCTGCGGGGCATGTTCACGATCAATTCCATT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               367 GGTCGGCTTGCCTTCATCCTGAATCCATGCACGACGCTCTAGCGCCCATCTTCAGGATC 426
sex-mixed), (tissue_type=hippocampus, dev_stage=adult,
sex=male), (tissue_type=whole body, dev_stage=9 days
embryo, sex=mixed), (tissue_type=lung, dev_stage=13 days
embryo, sex=mixed),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Overton, L., Russell, D., Chen, D., Riggs, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AIGGCCAGCGCCCAGGTICCTTTCTCCTTTGCCCCACTTCCTCATCTTTGTCTTC
                                                                                                                                                                                                                                                                                                                                                                                                         GTGACTTCCACCATCATCCACCTCCAGCAGCGAATAGTGAAGCTCCAACCCCTGTCAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 AAGGAATTACCGATGACGACTCAAATGTCCTCGGGAAACACAGAAAGCCCAGAGATGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCCGCCTGGGGAACCAGATGGGCGAATACGCCACACTCTTTGCACTGGCCAGGATGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvar,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Rigglong,P. and Fraser,C.M.

Rat BAC End Sequences from Library CHORI-230 EcoRI segment Unpublished (199)
Chfer_GSS: CH280_23110.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                            21;
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Clones are derived from the rat BAC library CHORI-230
                                                                                                                                                                                         Length 440;
                                                                                                                                                                                                                                               40; Indels
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Fax: 301 838 0208
Email: schoottigr.org
                                                                                                                                                                                         Score 243; DB 10;
Pred. No. 2.5e-56;
0; Mismatches 40;
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                                                                                       sex=mixed)
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Akimura, T. Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,

Hayasta, N., Hiranoka, T., Imotani, K., Ishii,

Hayasta, M., Hiranoka, T., Thio, T., Imotani, K., Ishii,

Y., Ito, M., Kawai, J., Nojima, Y., Konno, H., Kouda, M., Matsuyama, T.,

Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,

Salto, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,

Shidata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Kahira, S., Tanaka, T., Tomaru, A., Toya, T.,

Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

RIKEN Encyclopedia of Mouse Full-length CDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                               BB849545 BIKEN full-length enriched, adult inner ear Mus musculus cDNA clone F930101E05 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: genome_res@gsc.riken.go.jp,
URL:http://genome_gs.gsc.riken.go.jp,
Carnioci.p., Shibata,Y., Haytsu,N., Sugahara,Y., Shibata,K., Itoh
Carnioci.p., Shibata,Y., Haytsu,N., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matahiki,M., Yoneda,Y., Ishikwa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
Tel: 81-45-503-922
Fax: 81-45-503-9216
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIKEN integrated sequence analysis (RISA) system--384-format
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(tissue_type=cerebellum, dev_stage=0 day neonate,
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/note="pooled tissues ; (tissue_type=cerebellum
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/clone="F930101E05"
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1 (bases 1 to 522)
Kim, N. S., Hahn, Y., Oh, J. H., Lee, J. Y., Ahn, H. Y., Chu, M. Y., Kim, M. R., Oh, K. J., Cheong, J. E., Sohn, H. Y., Kim, J. M., Park, H. S., Kim, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BM773356 52SNU16s1 Homo sapiens cDNA clone S3SNU16s1-17-H05 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 GGCATCCGTCCTCGTACCTAIGTGGGTGTTCACGTGGTCGTCGTGGAGACTCTTTGGAGGTG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGCCTAATGTGTGGAAGGGCGTGGTGGCTGACCGGGGTTACCTGGAAAAGGCCCTGGAT 717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 IGGITCCGGGCCCGGCACAAAGACCCCATCITTGTGGTCACCAAGCAATGGCATGAGATGG 237
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                                                                                                                                                                                  /sex="Female"
/cell_type="Brain"
/rotl="Yetch: prarBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SSNHSd/MCW) BAC library produced by
Pieter de Jong"
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Korea Research Institute of Bioscience & Biotechnology
52 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea
                                                                                                                                                                                                                                                                                                                                       20.2%; Score 232.2; DB 17; Length 74.8%; Pred. No. 2.5e-53; ive 0; Mismatches 98; Indels
                                                                                                                             /db_xref="taxon:10116"
/clone="CH230-23L10"
/clone_lib="CHORI-230 Segment 1"
                                                                                          /organism="Rattus norvegicus"
//strain="BN/SsNHsd/MCW"
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21C Frontier Korean EST Project 2001
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Contact: Kim YS
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/note="Organ: Stomach; Vector: pTz18RP1; Site_1: ECORI; Site_2: Not1; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatuse (BAP) and then decapped with tabacco acid pyrophosphatuse (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including ECOR is the by treatment of 4 RNA ligase and the first strand CDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60Ht. The CDNA vector was circularized with E. coli DNA ligase after digestion of ECORI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The converted to a DNA strand by Okayama-Berg method. The converted to a DNA strand by Okayama-Berg method are obtained cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 - 3,000 colonias in original cDNA library, the abundant cDNAs library. After analyzing and sequencing about 2,000 - 3,000 colonias in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5 primer and N(dT)14 as 3 primer. The PCR products were used as template for synthesis of blotinylated single stranded cDNAs propered from original libraries were constructed by transformation of the remaining DNA into competent cells E. coli ToplOF' with electroporation method."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 CACCATCATCCACCTCCAGCAGCGAATAGTGAAGCTCCAACCCCTGTCAGAGGAATT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    278 GGGGAACCAGATGGGGGAGTACGCCACACTGTACGCCCTGGCCAAGATGAACGGGCGGCC 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309 IGCGTÚCATOCOCGCATOCATGCACAACGCTCTAGCGCCCCATOTTCAGGATCAGCCTCCC 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89
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Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
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                                                                                                     Plate: 17 row: H column: 05
High quality sequence stop: 522.
Location/Qualifiers
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17-22 Suehiro-Cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
Fax: 81-45-503-922
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
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Hayashizaki,Y.
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Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Harancho,K., Hirancka,T., Hirozane,T. Imotani,K., Ishii, Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Salto,R., Sakai,C., Sakai,C., Sakai,C., Sakai,K., Sakai,C., Sakai,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaka-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al. EST 26-NOV-2001 450 505 601 661 721 623 781 Laboratory for Genome Exploration Research Group, RIKEN Genomic Schones Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Isurumi-ku, Yokohama, Kanagawa 230-0045, Japan 436 bp mRNA linear EST 26-NOV-200 BB848859 RIKEN full-length enriched, adult inner ear Mus musculus CDNA clone F930004014 5', mRNA sequence. 331 CACAACGCTCTAGCGCCCATCTTCAGGATCAGCCTCCCGGTGTTACACAGGGACACGGC 662 CCAACCTCCGCCAGGAGATCCTTCCAGGAGTTCACCTGCAACGACCACCACGTGCGCGAGGA 542 AGCAGGAICCCCIGGCAGAACTACCACCIGAACGACTGGAIGGAGGAGGAGIACCGCCAC 451 ATTCCGGGACACT-TTGTGCGCTTCACGGGAT-ACCCGTGCTCCTGGACCT---TCTACC 506 ACCACCTGCGCCCAGAGAICC-TGAAGGAGITCACCCTGC-ATGACCACGIGCGGGAGGA 624 TGTCCATGTGCGCCGAGGGGACTATGTGCATGT Unpublished (2001) Contact: Yoshihide Hayashizaki

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and 137 c 98 g 94 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230 AAGGAATTAC---AGGCGGTTCAAATGTCCTCACCAAAGGGGGCAAGAACAGACAT--- 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 CGGGACAGCGAGCATGGGAATGGAGGCTGCGGGGCATGTTCACGATCAATTCCATT 240
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encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . il (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Matches 285; Conservative
                                                                                                      e mouse tissues.
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Search completed: May 26, 2003, 13:09:21 Job time : 1892.5 secs

Run on:

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1050.630 Million cell updates/sec
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- 2003 C
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
GenCore
Copyright (c) 1993
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		Rat hepatoma H35 c		henatoma	heratoma	Doroine secretor +	Dia secretor Cus	Himbo Cool Drotein	HINDAY COOK TRANSPORT	GNP-Firetheta-Fra	GDP-L-fucose-beta-
SUMMARIES		AAB36104	AAE16622	AAB36105	AAE16623	AAW37855	AAW53101	AAW69332	AAB36106	AAR13751	AAR80154
DB	1	21	23	21	23	16	5	5	21	12	16
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% Query Match		100.0	100.0	93.3	93.3	73.9	73.9	73.1	72.6	52.0	52.0
Score	1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0	2032	2032	1896	1896	1502	1502	1485.5	1475	1057.5	1057.5
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ALIGNMENTS

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Rat; alphal-2fucosyltransferase; cytostatic; neuroprotective; nootropic; gene therapy; Fucalphal-2Galbetal-3GalNAc; immunotherapy; immunosuppression; cancer; neurological disease; small cell lung carchoma.
                                                                            Rat hepatoma H35 cell alphal-2fucosyltransferase.
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                                                                                                                                                                                                             99WO-US07384.
                                                                                                                                                                                                                              99WO-US07384
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                                                                                                                                                                                                                                                                      Holmes EH, Sherwood AL;
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N-PSDB; AAC67965.
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                                                                                                                                                                                                            23-APR-1999;
                                                                                                                                                                                                                              23-APR-1999;
                                                         19-FEB-2001
                                                                                                                                                                                        02-NOV-2000.
                                     AAB36104;
RESULT 1
         AAB36104
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New rat ganglioside GM1-specific alphal-2Fucosyltransferase, useful for

a

location/Qualifiers

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                                                          The present sequence was given in a specification relating to an isolated trat gangloside GM. I: specific alphal-2fucosyltransferase protein. The protein or its cellular fraction is useful for synthesis of a molecule comprising Fucalphal-2Galbetal-3GalNAC, a glycolippid, glycoprotein, glycolipportein or a free oligosaccharide comprising glycoprotein or a free oligosaccharide comprising propertien or a free oligosaccharide comprising alphal-2Galbetal-3GalNAC. The method involves contacting alphal-2Galbetal-3GalNAC. The method involves of a molecule or glycolippid, glycolipprotein or oligosaccharide having a terminal by contacting the protein with GDP-fucose and ganglioside GM. The by contacting the protein with GDP-fucose and ganglioside GM. The oligosaccharides are useful as nutritional compositions and fucosyl-GM. I suseful for inducing an immunocherapeut. Or immunosuppressive action against cancer, neurological disease or small cell lung carcinoma.
  useful as a nutritional composition neurological diseases -
                                                                                                                                                                                                                                                                                                                                                                       61 RDSEQHGNGELRGMFTINSIGRLGNOMGEYATLFALARMNGRLAFIPASMHNALAPIFRI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                    180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TFGIWAAXLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLKALTPACP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat; alphal-2fucosyltransferase; alphal-2FucT; antisense therapy; galactose betal-3N-acetylgalactosamine; Galbetal-3GalNAc; glycolipid; glycoprotein; glycolipoprotein; oligosaccharide; fucosyl-GMI; cancer; gene therapy; oncogenic transformation; cytostatic; ganglioside; GMI;
                                                                                                                                                                                                                                                                                                                       1 MASAQVPFSFPLAHFLIFVFVTSTIIHLQQRIVKLQPLSEKELPMITQMSSGNTESPEMR 60
                                                                                                                                                                                                                                                                                                                                           1 MASAQVPFSFPLAHFLIFVFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMR 60
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      SLPVLHSDTAKKIPWQNYHLNDWMEBRYRHIPGHFVRFTGYPCSWTFYHHLRPBILKEFT
                                                                                                                                                                                                                                                                                                                                                                                     LHDHVREBAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM
                                                                                                                                                                                                                                                                                                                                                                                                                        SLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFT
                                                                                                                                                                                                                                                                       Score 2032; DB 21; Length 380;
Pred. No. 1.7e-212;
Mismatches 0; Indels 0;
preparation of fucosyl GM1 which is or immunotherapeutic for cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H35 cell alphal-2FucT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE16622 standard; Protein; 380 AA.
                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                        100.0%;
                                  Claim 1; Fig 5; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RSHFHLKAKGVICYVAGRAF 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RSHFHLKAKGVTCYVAGRAF 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  yene therapy; oncog
cell transformation
                                                                                                                                                                                                                                                380 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat hepatoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-APR-2002
                                                                                                                                                                                                                                                                                                 380;
                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                    Best Loca
Matches
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The invention relates to rat GMI-specific alphal-2fucosyltransferase
(alphal-2FucT) enzyme and its corresponding nucleic acid. This nucleic
acid is specific for a carbohydrate moiety found in gangiloside GMI,
acid is specific for a carbohydrate moiety found in gangiloside GMI,
acid is specific for a carbohydrate moiety found in gangiloside GMI,
acid is specific for a carbohydrate moiety found in gangiloside GMI,
saccharide. Alphal-2FucT DNA is useful for producing rat alphal-2FucT
protein by recombinant techniques. Alphal-2FucT DNA is useful for the
preparative synthesis of fucosyl containing glycolippids, glycolproteins,
glycolipoproteins and oligosaccharide, and for preparing fucosyl-GMI.
Alphal-2FucT DNA is useful for detecting oncogenic transformation which
involves assaying for changes in expression of alphal-2 FucT. Since
alphal-2FucT is activated in cell transformation, antisense sequences
derived from alphal-2FucT DNA is useful in gene therapy and
cor treating cancer. Alphal-2FucT DNA is useful in gene therapy and
cor treating cancer harbal-2FucT DNA is useful in gene therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat hepatoma H35 cell alphal-2fucosyltransferase, useful for producing GMI-specific alphal-2fucosyltransferase enzyme by recombinant techniques and for detecting oncogenic transformation of test tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RDSEQHGNGELRGMFTINSIGRLGNQMGEXATLFALARMNGRLAFIPASMHNALAPIFRI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 LHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM
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                               /note= "Intracellular/Transmembrane domain"
199
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/note= "Region which overlaps rat
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                                                                                                     "N-glycosylated"
                                                                                                                                                                                                                                                                       /note= "N-glycosylated"
                                                                                                                                                                                                                      /note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Fig 5; 41pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-029886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NWHO-) NORTHWEST HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002-121132/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      380 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAD27207
                                                                           Modified-site
                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                             Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-APR-1999;
                                                                                                                                                                                                                                                                                                                        US6329170-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         380;
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Key
Domain
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241 FRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIG 300

301 301 361 361

qq QΥ

δŏ Db RESULT 3 AAB36105

207 180 267 327

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Rat hepatoma H35 cell alphal-2fucosyltransferase, useful for producing GM1-specific alphal-2fucosyltransferase enzyme by recombinant techniques and for detecting oncogenic transformation of test tissues
                                                                                                                                                                                                                                     Rat; alphal-2fucosyltransferase; alphal-2fucT; antisense therapy; galactose betal-3N-acetylgalactosamine; Galbetal-3GalNac; glycolipid; glycoprotein; glycolipoprotein; oligosaccharide; fucosyl-GM1; cancer; gene therapy; oncogenic transformation; cytostatic; ganglioside; GM1;
                    GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER
                                                                                                                                         GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS
                                                                                                                                                                                                               RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF
                                                                     YRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFV
                                                                                                                                                            LKVFKPEAAFLPEWVGIPADLSPLLKALIPACPRSHFHLKAKGVTCYVAGRAF 380
                                                                                                                                                                                                                                                                                                       /note= "Region which overlaps rat FTB"
238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H35 cell alphal-2FucT catalytic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "N-glycosylated"
266
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/note=_"N-glycosylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell transformation; catalytic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                     AA.
                                                                                                                                                                                                                                                                                                                                                                                                             AAE16623 standard; Protein; 353
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292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus.
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat hepatoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-APR-2002
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88
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AAE16623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New rat ganglioside GMI-specific alphal-2Fucosyltransferase, useful for preparation of fucosyl GMI which is useful as a nutritional composition or immunotherapeutic for cancer and neurological diseases -
       TFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLKALTPACP 360
                          Rat; alphal-2fucosyltransferase; cytostatic; neuroprotective; nootropic; gene therapy; Fucalphal-2Galbetal-3GalNAc; immunotherapy; immunosuppression; cancer; neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.3%; Score 1896; DB 21
100.0%; Pred. No. 1e-197;
Live 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PACI-) PACIFIC NORTHWEST CANCER FOUND.
                                                                                                                                                                                                             AA.
                                                                                                                                                                                                           AAB36105 standard; Protein; 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Fig 3A; 91pp; English.
                                                                                                   RSHFHLKAKGVTCYVAGRAF 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US07384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US07384
                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                             small cell lung carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 353; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sherwood AL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-687262/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        353 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAC67966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200064464-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-APR-1999;
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                                                                                                                                                                                                                                                                               19-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Holmes EH,
                                                                                                                                                                                                                                             AAB36105;
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Sequence

28

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The invention relates to rat GMI-specific alphal-2fucosyltransferase (alphal-2FucT) enzyme and its corresponding nucleic acid. This nucleic acid is specific for a carbohydrate moiety found in ganglioside GMI, a terminal galactose betal-3W-acceptygalactosamine (Galbetal-3GalNac) saccharide. Alphal-2FucT DNA is useful for producing rat alphal-2FucT protein by recombinant techniques. Alphal-2FucT DNA is useful for the preparative synthesis of fucosyl containing glycolipids, glycoproteins, glycolipoproteins and oligosaccharide, and for preparing fucosyl-GMI. Alphal-2FucT DNA is useful for detecting oncogenic transformation which involves assaying for changes in expression of alphal-2FucT. Since alphal-2FucT DNA are useful for inhibiting, suppressing criticating cancer. Alphal-2FucT DNA is useful in gene therapy and antisense therapy. The present sequence is rat hepatoma H35 cell
                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268 RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIXLANYTLPDSPF 327
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                  87
                                                                                                                                                                                                                                                                                                                                                                                                  LQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YRHIPGHFVRFIGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF
                                                                                                                                                                                                                                                                                                                                                 .;
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    328 LKVFKPEAAFLPEWVGIPADLSPLLKALTPACPRSHFHLKAKGVTCYVAGRAF 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 LKVFKPEAAFLPEWVGIPADLSPLLKALTPACPRSHFHLKAKGVTCYVAGRAF 353
                                                                                                                                                                                                                                                                                                              Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Secretor; glycosyltransferase; FUT2; pig; epitope; antigen; transgenic animal; xenotransplantation; organ transplant.
                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "N-terminal cytoplasmic tail"
                                                                                                                                                                                                                                                                                                          93.3%; Score 1896; DB 23;
100.0%; Pred. No. 1e-197;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "C-terminal domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Porcine secretor transferase (FUT2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW37855 standard, Protein, 340 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                            Matches 353; Conservative
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185..187
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                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                            353 AA;
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                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                               Best Local
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This polypeptide comprises porcine secretor glycosyltransferase

(SE or FUI2), a type II integral membrane protein has high affinity

(SE or FUI2), a type II integral membrane protein has high affinity

(SE or FUI2), a type II integral membrane protein has high affinity

(Cor type I and type III substrates. Its amino acid sequence was

deduced from the nucleotide sequence of a genomic DNA clone (see

AAV29003) isolated from a pig Ilver library on the basis of homology

Cor human FTD2 cDNA. Pig FUIZ shows 83.2% identity with human FUIZ.

Expression of a glycosyltransferase, such as porcine Se, in a

tissue results in reduced expression of unwanted carbohydrate

c pitopes on the tissue, especially porcine heart, liver, kidney or

pancreas, rendering if more suitable for transphantation, i.e. less

immunogenic and of increased immunological acceptability. A

claimed method of producing a cell from a donor species that is

immunologically acceptable to a recipient species sinvolves reducing

levels of carbohydrate on the donor cell that causes it to be

recognised as non-self by the recipient by expressing a nucleic

acid for a glycosyltransferase such as porcine Se in the cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MASAQVPFSFPLAHFLIFVFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RDSEQHGNGELRGMFTINSIGRLGNQMGEXATLFALARMNGRLAFIPASMHNALAPIFRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 SLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 -----SSPQLKGMWTINAIGRLGNQMGEYATLYALARMNGRPAFIPPEMHSTLAPIFRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MLSMQASFFFPTGPFILFVFTASTIFHLOORMVKIOP--TWELOMVTOVT---TESP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 LHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIG
                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding glycosyltransferase able to compete with second such enzyme - particularly used to reduce expression of unwanted carbohydrate epitope(s) on tissues intended for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 TFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGÌPADLSPLLK 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         287 TFGIWAAYLAGGETIYLANYTLPDSPFLKLFKPEAAFLPEWIGIEADLSPLLK 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.9%; Score 1502; DB 19;
79.6%; Pred. No. 9.1e-155;
iive 28; Mismatches 30;
                   /note= "Asn is N-glycosylated" 305..307
                                                             /note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Fig 1A-B; 40pp; English.
                                                                                                                                                                                         97WO-AU00540.
                                                                                                                                                                                                                                   96AU-0001823,
                                                                                                                                                                                                                                                                                                                     Sandrin MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 73.99
Best Local Similarity 79.67
Matches 281, Conservative
  279..281
                                                                                                                                                                                                                                                                         (AUST-) AUSTIN RES INST.
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                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAV29003
Modified-site
                                                                                                                                                                                                                                                                                                                   McKenzie IFC,
                                         Modified-site
                                                                                                                                                                                                                                   23-AUG-1996;
                                                                                                     W09807837-A1
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This sequence is the human Sec2 protein of the invention. The DNA encodes a alpha(1,2) fucosyltransferase and is the Secretor alpha(1,2) fucosyltransferase locus, that cross hybridises with the H blood group alpha(1,2)fucosyltransferase gene. The DNA is useful for producing a recombinant human GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase (FUT2) which can be used for genotyping an individual as a secretor or nonsecretor as it is known that nonsecretors homozygous for a mutant allele of the FUT2 gene that has a stop codon in the position corresponding to amino acid 143.
                                                                                                                                                                                                                                                                                                                                                                                Sec2; alpha(1,2) fucosyltransferase; H blood group; secretor genotyping; GDP-L-fucose;beta-D-galactoside 2-alpha-L-fucosyltransferase; human;
                       PRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STSKALGPSQLRGMWIINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRI 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MASAQVPFSFPLAHFLIFVFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 19; Length 343;
                                                                                                    TFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK
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77.9%; Pred. No. 5.8e-153;
ive 30; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            secretor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - nseful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            recombinant enzyme and genotyping person as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lowe JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Column 45-50; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding fucosyltransferase enzyme
                                                                                                                                                                                                                     AAW69332 standard; Protein; 343 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lennon G,
                                                                                                                                                                                                                                                                                                                                                                                                                          FUT2; nonsecretor genotyping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-0395800.
                                                                                                                                                                                                                                                                                                                                           Human Sec2 protein sequence.
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                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 73.1
Best Local Similarity 77.9
Matches 275; Conservative
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KELLY R J.
LENNON G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAV58323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-1995;
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                                                                               δy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents pig secretor used in an example of the present invention. The present invention describes nucleic acids (NA) encoding a chimeric glycosyltransferase. The NAs comprises a catalytic domain of a first glycosyltransferase (GT) and a localisation signal of a second GT, whereby when the NA is expressed in a cell and where the commerce as located in an area of the cell where it is able to compete for substrate with a second GT, resulting in reduced levels of a product from the second GT. The NAs can be used to produce cells and organs with desired glycosylation patterns. Products and methods of the present invention can be used to reduce the levels of undesirable epitopes in cells, tissues or organs which may be used in transplantation or gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIFASMHNALAPIFRI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MASAQVPFSFPLAHFLIFVFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MLSMQASFFFPTGPFILFVFTASTIFHLQQRMVKIQP--TWELQMVTQVT---TESP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding chimeric glycosyltransferases - used for altering carbohydrate levels on the surface of cells, useful in therapy and transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 340;
                                                                                                                                                                                                                     chimeric; glycosyltransferase; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.9%; Score 1502; DB 19;
79.6%; Pred. No. 9.1e-155;
iive 28; Mismatches 30;
                                                        AAW53101 standard; Protein; 340 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Fig 6; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-0024279.
                                                                                                                                                                                                                                                                                                                                                                                                 97WO-AU00492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 73.9%
Best Local Similarity 79.6%
Matches 281; Conservative
                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sandrin MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AUST-) AUSTIN RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-159170/14.
N-PSDB; AAV21639.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               340 AA;
                                                                                                                                                                                                                                        transplantation.
                                                                                                                                                                                                                     secretor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McKenzie IFC,
                                                                                                                                                                                                                                                                                                                    WO9805768-A1
                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                       21-AUG-1996;
02-AUG-1996;
                                                                                                                                    08-JUL-1998
                                                                                                                                                                                                                                                                                                                                                            12-FEB-1998
                                                                                                                                                                                                                                                                              Sus scrofa.
                                                                                                AAW53101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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Pred. No. 8.1e-152;
); Mismatches 37;
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AAR23751 standard; Protein; 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90US-0627621.
90US-0479858.
90US-0480133.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
               Best Local Similarity 77.7
Matches 275; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UNMI ) UNIV OF MICHIGAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1991-267151/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAR13751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-FEB-1990;
14-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2-DEC-1990:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9112340-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR13751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lowe JB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is given in a specification relating to a rat ganglioside GM_1-specific alphal-2fucosyltransferase protein. The protein or its cellular fraction is useful for synthesis of a molecule comprising Fucalphal-2Galbetal-3GalNRo. a glycolpid, glycoprotein, glycolipoprotein or a free oligosaccharide comprising Fucalphal-2Galbetal-3GalNRo. The method involves contacting alphal-2fucosyltransferase with GDP-fucose and a molecule or glycolipid, glycoprotein, glycolipoprotein oligosaccharide having a terminal Galbetal-3GalNac group. It is also oligosaccharide having a terminal Galbetal-3GalNac group. It is also oligosaccharide having a terminal Galbetal-3GalNac group. It is also glycolipose and ganglioside GM_1. The obtained glycoproteins, glycolipids and oligosaccharides are useful as nutritional compositions and fucosyl-GM_1 is useful for inducing an nutritional compositions and fucosyl-GM_1 is useful for inducing an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New rat ganglioside GMI-specific alphal-2Fucosyltransferase, useful for preparation of fucosyl GMI which is useful as a nutritional composition or immunotherapeutic for cancer and neurological diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; Sec2; alphal-2fucosyltransferase; cytostatic;
neuroprotective; nootropic; gene therapy; Fucalphal-2Galbetal-3GalNAc;
immunotherapy; immunosuppression; cancer; neurological disease;
                                               240
                                                                                                                                                                                         FRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIG 300
                          SLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFT 180
                                                                                                                        LEDHVREBAQKFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDW
                                                                                               LHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM
                                                                                                                                                                                                                                                  353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunotherapeutic or immunosuppressive action against cancer, neurological disease or small cell lung carcinoma.
                                                                                                                                                                                                                                                                  TFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.6%; Score 1475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PACI-) PACIFIC NORTHWEST CANCER FOUND.
                                                                                                                                                                                                                                                                                                                                                                         AAB36106 standard; Protein; 344 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example; Fig 3B; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Sec2 catalytic domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US07384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US07384
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            small cell lung carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Holmes EH, Sherwood AL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-687262/67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200064464-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                19-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                                           AAB36106;
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230 WFRARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTI 289
                                                                                                                                                                                                      RDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRI 120
                                                                                                                                                                                                                                                   50 STSKALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRI 109
                                                                                                                                                                                                                                                                                                                                                    SLPVLHSDTAKKIPWQNYHLNDWMEERYRHI-PGHFVRFTGYPCSWTFYHHLRPEILKEF 179
   Gaps
                                                               MASAQVPFSFPLAHFLIFVFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMR 60
                                                                                                                               MLVVQMPPSFPMAHFILFVFTVSTIFHVQQRLAKIQAM--WELPV------QIPVLA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The amino acid sequence codes for a protein capable of functioning as a GPP- Fuc:[beta-D-Gal alpha(1,2)- fucosyltransferase. The functional protein is represented by amino acids 33 to 365. The enzyme produced by the DNA sequence can be used in enzymatic fucosylation of chain-terminating galactose residues on lactosemine or neolacto type beta-D-galactoside to alpha-2-L-fucose residues. See also AARI3749-R13752.
                                                                                                                                                                                                                                                                                                                                                                                          180 TLHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 MFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           343
12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTFGIWAAYLTGGDIIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLK
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Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GDP-Fuc:beta-D-galactoside alpha(1,2)-fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolation of gene conveying post-translational e.g. the presence of soluble or membrane bound polysaccharide or glycosyltransferase.
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GDP-L-fucose-beta-D-galactoside 2-alpha-fucosyl-transferase (Fuc-T) is encoded by cDNA (AAQ98461) isolated from a human epidermal carcinome cell line. The enzyme is responsible for the synthesis of 2'-fucosyllactose, one of the oligosaccharides in human milk. Other products of Fuc-T include glycoprotiens contg. beta-linked terminal galactose residues which can be fucosylated by Fuc-T. This DNA can be used to produce non-human transgenic mammals able to produce secondary gene products, e.g. oligosaccharides, in their milk. The transgenic mammals milk biochemically resembles human milk. This humanised milk can be used in the prepn. of an enteral nutritional product useful in the nutritive maintenance of an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 IPRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEIL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                               -----QH-PASLSGIWTVYPNGRFGNQMGQYATLLALAQLNGRRAFILPAMHAALAP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 KEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWYGIPADLSPLLKA 354
                                                                                                                                                                                                                                                                                                                                                --RIVKLQPLSEKELPMTTQMSSGNTES 56
                                                                                                                                                                                                                                                                                                                                                                           11 LAFLLVCVLSVIFFLHIHODSFPHGLGLSILCPDRRLVIPPVAIFCLPGTAMGPNASSSC
                                                                                                                                                                                                                                                                                                                                                                                                              57 PEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glycosyltransferase; glycosylation; oligosaccharide; glycoprotein; glycolipid; transgenic animal; cattle; milk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDP-L-fucose-beta-D-galactoside 2-alpha-fucosyltransferase;
                                                                                                                                                                                                                                                                                                              87; Indels
                                                                                                                                                                                                                                                                               DB 16;
                                                                                                                                                                                                                                                                       52.0%; Score 1057.5; DB 18 56.5%; Pred. No. 3.1e-106; iive 46; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR70422 standard; Protein; 365 AA
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                                                                                                                                                                                                                                                                                          Best_Local Similarity 56.5
Matches 205; Conservative
                                                                                                                                                                                                                                                                                                                                             12 LAHFLIFVFVTSTIIHLQQ-
                                                                                                                                                                                                                                        365 AA;
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                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                           71 P-----QH-PASLSGTWFVYPNGRFGNQMGQYATJLALAQINGRRAFILPAMHAALAP 122
                                                                                                                                                                                                                                        117 IFRISLPVLHSDTAKKIPWQNYHLNDWMEBRYRHIPGHFVRFTGYPCSWTFYHLRPEIL 176
                                                                                                                                                                                                                                                                  177 KEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYL 234
                                                                                                                                                                                                                                                                                                                                                                                   235 EKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNH 294
                                                                                                                                                                                                                                                                                                                                                                                                     243 RQAMDWFRARHEAPVFVVTSNGMEWGKENIDTSQGDVTFAGDGQEATPWKDFALLTQCNH 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                    295 TIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWGIPADLSPLLKA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GDP-L-fucose-beta-D-galactoside 2-alpha-fucosyl-transferase; Fuc-T; synthesis; 2'-fucosyllactose; oligosaccharide; human milk; non-human transgenic mammal; secondary gene product.
                                                                                                                           57 PEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATJFALARMNGRLAFIPASMHNALAP
                                                                                                         ----RIVKLQPLSEKELPMTTQMSSGNTES
                                                                                                                                                                                                                                                                                                                                     Prodn. of human:ised milk by non-human transgenic mammal - by inserting heterologous gene encoding human catalytic entity which produces oligo:saccharide(s) and glyco:conjugate(s) into mammal's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDP-L-fucose-beta-D-galactosidase alpha-1,2-fucosyltransferase.
                                         Length 365;
                                                                      87; Indels
                                    DB 12;
                                    ; Score 1057.5; DB 12; Pred. No. 3.1e-106; 46; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mukerji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Moreman KW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 62-54; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; Protein; 365 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith DF;
                                    52.0%;
56.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95WO-US00926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94US-0209122
                             Query Match
Best Local Similarity 56.5
Matches 205; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                     LAHFLIFVFVTSTIHLQQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kopchik JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prieto PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1995-336739/43.
 365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAQ98461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cummings RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           355 LTP 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9524494-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pierce JM,
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR80154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR80154
                                                                                                     12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363
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AAR80154

11.6

7.0

Length 365;

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57 PEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAP 116
                                                                                                                                                                                                                                                                                                                                                                                                                           IFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEIL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - contg. heterologous
                                                                                                                                                                                                                                                                                               25; Gaps
                                                                                                                                                        2-Alpha-fucosyltransferase (AAR70422) is encoded by a cDNA clone (AAR01083) isolated from a human epidermal carcinoma A431 library. The enzyme can be expressed in the milk of a transgenic mammal, esp. cow. This allows large-scale prodn. of oligosaccharides and glycosylated proteins and lipids in the milk.
                                                                                                                                                                                                                                                                                                                                            11 LAFLLVCVLSVIFFLHIHQDSFPHGLGLSILCPDRRLVTPPVAIFCLPGTAMGPNASSSC
                                                                                                                                                                                                                                                                                                                                                                                          KEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFILHDHLEREAQSVLGQLRLGRTGDRPRTFVGVHVRRGDYLQVMPQRRKGVVGDSAYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLKA
                                                                                                                                                                                                                                                                                                                    12 LAHFLIFVFVTSTIIHLQQ------RIVKLQPLSEKELPMTTQMSSGNTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDP-L-fucose-beta-D-galactoside 2-alpha-fucosyltransferase; glycosyltransferase; oligosaccharide; glycoprotein; glycolipid; transgenic animal; cattle; glycosylation; milk.
                                                                                                                                                                                                                                                                    16; Length 365
                                                                                                                                                                                                                                                                                               87; Indels
                                                                                                                                                                                                                                                                  52.0%; Score 1057.5; DB 16 56.5%; Pred. No. 3.1e-106; iive 46; Mismatches 87;
               Mukerji
                                                                                                        components produced as secondary gene prods.
                                                                                          mammal milk prods
             Moremen KW,
                                                                                                                                Example 1; Page 62-64; 83pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR70421 standard; Protein; 365 AA.
                           Smith DF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2-Alpha-fucosyltransferase
            Kopchik JJ,
                                                                                                                                                                                                                                                                              Best Local Similarity Ju., Matches 205; Conservative
                                                                                            New transgenic non-human
             Cummings RD, Kopchik J
Pierce JM, Prieto PA,
                                                   WPI; 1995-328284/42.
                                                                                                                                                                                                                                        365 AA;
                                                                 N-PSDB; AAT01083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9524488-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTP 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AKP 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-FEB-1996
                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR70421;
                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                           117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183
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117 IFRISLPVLASDTAKKIPWQNYHLNDWMEBRYRHIPGHFVRFTGYPCSWTFYHHLRPEIL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 354
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      ---RIVKLOPLSEKELPMTTQMSSGNTES 56
                                                                                                                                                                                                                                                            Alpha-1,2-fucosyltransferase (AAR70421) is encoded by a cDNA clone (AAT01082) isolated from a human epidermal carcinoma cell line A431 cDNA library. The enzyme can be expressed in the milk of a transgenic mammal, esp. cow. This allows large-scale prodn. of oligosaccharides or glycosylated proteins and lipids in the milk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 RQAMDWFRARHEAPVFVVTSNGMEWCKENIDTSQGDVTFAGDGQEATPWKDFALLTQCNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 LAFLLVCVLSVIFFLHIHQDSFPHGLGLSILCPDRRLVTPPVAIFCLPGTAMGPNASSSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 KEFTLHDHVREEAQAFLRGLRY--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  295 TIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLKA
                                                                                                                                                                                                디
                                                                                                                                                                                                                                                                                                                                                                                                          25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H-transferase; xenograft hyperacute rejection; transplantation; glycosyltransferase; galactose alpha(1,3) galactose.
                                                                                                                                                        Transgenic animal expressing heterologous catalyst - used in metabolite prodn esp. glycosyltransferase for prodn. of oligosaccharide(s) and glyco-conjugate(s) in the milk, useful foods, pharmaceuticals, etc.
                                                                                                                                                                                                                                                                                                                                                                               DB 16; Length
                                                                                                                                                                                                                                                                                                                                                                                                          87; Indels
                                                                                                                                                                                                                                                                                                                                                                             52.0%; Score 1057.5; DB 1056.5%; Pred. No. 3.1e-106;
                                                                                                                                                                                                                                                                                                                                                                                                        46; Mismatches
                                                                                I, Moremen KW,
Smith DF;
                                                                                                                                                                                                                                    Example 1; Page 62-64; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein; 365 AA
                        94US-0209132
95WO-US01147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                               Kopchik JJ,
                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 56.5
Matches 205; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   LAHFLIFVFVTSTIIHLOO-
                                                                                               Prieto PA,
                                                                                                                        WPI; 1995-328279/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human H-transferase.
                                                    (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR90572 standard;
                                                                                                                                                                                                                                                                                                                                               365 AA;
                                                                                                                                      N-PSDB; AAT01082.
24-JAN-1995;
                        09-MAR-1994;
                                                                                Cummings RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    365
                                                                                               Pierce JM,
                                                                                                                                                                                                                                                                                                                                                  Seguence
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                                                                                                                                                                                                                                                                                                                                                                              Query Match
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qq
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us-10-040-863-8.rag

(first entry)

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15-SEP-1997
                                                                                                                                                        29-APR-1997
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                                                                                                                                                                                                                                    Falk P,
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      δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
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                                                                                                                                                                                                                                                                                                                                                         4;
                                                                                                                                                                                                                                     The human H-transferase (AAR90572) product of a cDNA clone (AAT12238) prepd. from human epidermoid carcinoma cells (ATCC CRL 155 A-431) can be expressed in xenogeneic organs, tissues and cells using a vector such as pAPEx-1 (AAT1239). This results in decreased expression of the non-human antigen galactose alpha(1.3) galactose on the surface of the organs etc. so that hyperacute rejection is reduced upon transplantation to humans.
                                                                                                                                                                                                                                                                                                                                                                                                            57 PEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAP 116
                                                                                                                                                                                                                                                                                                                                                                                                                         117 IFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPBIL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNH 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLKA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 LAFLLVCVLSVIFFLHIHQDSFPHGLGLSILCPDRRLVTPPVAIFCLPGTAMGPNASSSC 70
                                                                                                                                                                                                                                                                                                                                                                          -----RIVKLQPLSEKELPMTTQMSSGNTES 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 KEFTLHDHVREBAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYL
                                                                                                                                                                         Redn. of rejection of xenogeneic cells following transplantation by introducing a vector expressing fucosyl:transferase into the cells
                                                                                                                                                                                                                                                                                                                                   52.0%; Score 1057.5; DB 17; Length 365; 56.5%; Pred. No. 3.1e-106; live 46; Mismatches 87; Indels 25;
                                                                                                                                     Squinto SP;
                                                                                                                                   Sandrin MS,
                                                                                                                                   Rother RP,
                                                                                                                                                                                                                     Example 1; Page 45-47; 69pp; English.
                                                        95WO-US07554
                                                                           94US-0278282
                                                                                    94US-0260201
                                                                                                     (ALEX-) ALEXION PHARM INC. (AUST-) AUSTIN RES INST.
                                                                                                                                                                                                                                                                                                                                                                       12 LAHFLIFVFVTSTIIHLQQ-
                                                                                                                                 Mckenzie IFC,
                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                    WPI; 1996-049326/05
                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                 365 AA;
                                                                                                                                                            N-PSDB; AAT12238
                                                                          21-JUL-1994;
                                                                                   L5-JUN-1994;
                 WO9534202-A1
                                                       14-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      355 LTP 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AKP 365
                                    21-DEC-1995
                                                                                                                                                                                                                                                                                                                                                       205;
                                                                                                                                Fodor WL,
                                                                                                                                                                                                                                                                                                                  Seguence
                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                              Best Local
                                                                                                                                                                                                                                                                                                                                                     Matches
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ID AAW2
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AC AAW2
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A claimed transgenic mouse expresses, in its intestinal epithelial cells, the enzyme human GDP-L-fucose.beta-D-galactoside 2-alpha-L-fucosyltransferase (also called alpha 1.2 FT) or human GDP-L-fucose.beta-D-N-acetylglucosamide 3/4-alpha-L-fucosyltransferase (also called alpha 1.3/4 FT). The enzyme is expressed under the control of a qut epithelial cell-specific promoter and Helicobacter pylori adheres to the transgenic cells. The transgenic mouse and intestinal epithelial cells from it are useful as models for screening compounds for the ability to inhibit adhesion of H. pylori to gut epithelial cells. The present sequence represents human alpha 1.2 FT and was published by Larsen et al., Proc.Natl.Acad.Sci.USA, 87:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 PEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 P-----QH-PASLSGTWTVYPNGRFGNQMGQYATLLALAQLNGRRAFILPAMHAALAP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 IFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEIL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                          Human GDP-L-fucose:beta-D-galactoside-2-alpha-L-fucosyltransferase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Animal model for Helicobacter pylori infection - comprising transgenic mouse expressing human enzyme promoting intestinal
                                                                                      alpha 1,2 FT; transgene; transgenic mouse; animal model; intestinal adhesion; Helicobacter pylori infection; stomach; small intestine; gut; epithelial cell; surface receptor; carbohydrate antigen; gastritis; peptic ulcer; neoplasia; gastric adenocarcinoma; Lewis antigen; fucosylation.
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Human alpha 1,2 fucosyltransferase (EC 2.4.1.69).
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45; Mismatches 87;
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                                                                                                                                                                                                                                                                                                  Homo sapiens
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AAW23805 standard; Protein; 365 AA.

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              PEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAP 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human GDP-Puc:beta-D-galactoside alpha(1,2)-fucosyltransferase (AAW13640) is an enzyme involved in the expression of type I and II blood group H structures. Its amino acid sequence was deduced from an isolated DNA (AATG1677) derived from human A431 cells. Expression of the fucosyltransferase animal cell lines provides specific capabilities with respect to post-translational modification of the oligosaccharides of expressed proteins or lipids. Specific applns. of the enzyme include enzymatic fucosylation of chain-terminating galactose residues on lactoseamine or neolacto type beta-D-galactoside to alpha-2-fucose residues. The enzyme can also be used to raise antibodies as diagnostic reagents and to screen cpds. for fucosyltransferase inhibitor activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant fucosyltransferase proteins - useful for modifying cell surface oligosaccharide structures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.0%; Score 1057.5; DB 18; Length 365; 56.5%; Pred. No. 3.1e-106; Live 46; Mismatches 87; Indels 25;
                                                                                                                                                                                                                                                         Alpha(1,2)-fucosyltransferase; glycosylation; oligosaccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 280-281; 329pp; English.
                                                                                                                                                                                                                                Human alpha(1,2)-fucosyltransferase.
                                                                                                                                               AAW13640 standard; Protein; 365 AA.
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OM protein - protein search, using sw model

May 27, 2003, 15:03:22 ; Search time 15.6237 Seconds (without alignments) 715.625 Million cell updates/sec Run on:

Title: Perfect score:

US-10-040-863-8 2032 1 MASAQVPFSFPLAHFLIFVF......RSHFHLKAKGVTCYVAGRAF Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

262574 seqs, 29422922 residues Searched:

262574 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/cgn2_6/ptcdata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptcdata/1/iaa/5B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Sequence 33, Appl	Sequence 35, Appl	5	ø	C	Sequence 22, Appl	S		é	ω	w	'n	4	Seguence 6, Appli	6. Appl	é	3, Appl	4, Appl
-08-539-005-3	US-09-280-598-35	US-09-390-131-5	-349	US-08-220-151-22	US-08-413-118-22	US-08-473-446-22	5470718-3	0	US-08-208-887A-6	US-08-539-005-6	US-08-815-176-3	-	US-08-664-962B-6	US-09-311-743-6	US-09-280-598-6	US-09-197-344-3	US-09-197-344-4
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26	76	96.5	91.5	51	91	91	91	87	87	87	87	87	87	8.7	87	87	87
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Sequence 8, Application US/09298886 Sequence 8, Application US/09298886 Sequence 8, Application US/09298886 Sequence 8, Application US/09298886 Sequence 1 NFORMATION: TITLE OF INVENTION: GMI-SPECIFIC ALPH, TITLE OF INVENTION: THEREOF TITLE OF INVENTION: THEREOF TITLE OF INVENTION: THEREOF TITLE OF INVENTION: THEREOF STILE REPERENCE: 8511-029 CURRENT APPLICATION NUMBER: US/09/298 CURRENT APPLICATION NUMBER: US/09/298 CURRENT APPLICATION NUMBER: US/09/298 CURRENT APPLICATION NOWS: 29 SOFTWARE: PART ORGANISM: Rattus norvegicus 1 DO: 08; Pred. 109-298-886-8 SEQ LO O8 Best Local Similarity 100.08; Pred. MASAQVPESFPLAHFLIFVFVTSTITHLQQI 1 MASAQVPESFPLAHFLIFVFVTSTITHLQQI 1 MASAQVPESFPLAHFLIFVFVTSTITHLQQI 1 MASAQVPESFPLAHFLIFVFVTSTITHLQQI 1 MASAQVPESFPLAHFLIFVFVTSTITHLQQI 1 MASAQVPESFPLAHFLIFVFVTSTITHLQQI 1 ASSQVPESFPLAHFLIFVFVTSTITHLQQI 1 ASSQVPESFPLAHFLIFVFVTSTITHLQQI 1 ASSQVPESFPLAHFLIFVFVTSTITHLQQI 1 ASSQVPESFPLAHFLIFVFVTSTITHLQQI 1 ASSQVPESFPLAHFLIFVFVTSTITHLQQI 1 ASSQVPESFPLAHFLIFVTSTGRIGNOMGEYRI 1 ASSQVPESFPLAHFLIFITINI 1 ASSQVPESFPLAHFLIFITINI 1 ASSQVPESFPLAHFLIFITINI 1 ASSQVPESFPLAHFLIFITINI 1 ASSQVPESFPLAHFLIFVTSTGRINAGERYRH 1 ASSQVPESFPLAHFLIFITINI 1 A
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Similarity
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US-09-254-077A-6
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                                                                      Sequence 10, Application US/09298886
Fatent No. 632970
GENERAL INFORMATION:
TITLE OF INVENITON: GAL-SPECIFIC ALPHA1-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENITON: GAL-SPECIFIC ALPHA1-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENITON: THEREOF
FILE REFERENCE: 8511-029
CURRENT APPLICATION NUMBER: US/09/298,886
CURRENT APPLICATION NUMBER: US/09/298,886
NUMBER OF SEQ ID NOS: 29
SEQ ID NOS: 29
SEQ ID NOS: 29
LENGTH: 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120
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APPLICANT: SANDEIM, MAURO S.
TITLE OF INVENTION NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
FILE REPERENCE: 30562.508w0
CURRENT APPLICATION NUMBER: US/09/254,077A
CURRENT FILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: PCI/AUG/7/00540
PRIOR APPLICATION NUMBER: PO 1823
PRIOR PILING DATE: 1996-08-23
PRIOR FILING DATE: 1996-08-23
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Pred. No. 1.5e-210;
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100.0%;
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ORGANISM: Rattus norvegicus
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 361 RSHFHLKAKGVTCYVAGRAF
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ORGANISM: Sus scrofa
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61 RDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRI 120
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APPLICANT: SANDRIN, MAURO S.
APPLICANT: SANDRIN, MAURO S.
TITLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
TITLE REFERENCE: 3626.5508R
CURRENT APPLICATION NUMBER: US/09/254,077A
CURRENT FILING DATE: 1997-06-11
PRIOR FILING DATE: 1997-06-22
PRIOR FILING DATE: 1997-08-23
PRIOR FILING DATE: 1996-08-22
PRIOR FILING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                 1 MLSMQASFFFPTGPFILFVFTASTIFHLQQRMVKIQP--TWBLQMVTQVT---TESP---
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79.6%; Pred. No. 5.1e-165;
tive 28; Mismatches 30;
73.9%; Score 1502; DB 4;
79.6%; Pred. No. 5.1e-165;
iive 28; Mismatches 30;
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Best Local Similarity 79.69
Matches 281; Conservative
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CURRENT APPLICATION NUMBER: US/09/254,077A
CURRENT FILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: PCT/AU97/00540
PRIOR PILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: PO 1823
PRIOR FILING DATE: 1996-08-23
PRIOR FILING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN Ver: 2.1
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                                                                                                                                                                                       Sequence 8, Application US/09254077A
Patent No. 6399758
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ORGANISM: Homo sapiens
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US-09-254-077A-8
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APPLICANT: GIORGI, DOMINIQUE
TITLE OF INVENTION: 2-ALPHA-L-FUCOSE: BETA-D-GALACTOSIDE
TITLE OF INVENTION: SAME, METHOD FOR PRODUCING THE SAME AND A METHOD OF
TITLE OF INVENTION: GENOTYPING A PERSON
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
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                                   TFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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77.9%; Pred. No. 4.2e-163;
tive 30; Mismatches 37;
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28-FEB-1995
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                                                                                                                                                                                                          Sequence 8, Application US/08395800A
Patent No. 5807732
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IBM PC compatible
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TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 8:
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Best Local Similarity 77.99
Matches 275; Conservative
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FILING DATE: 28-FEB
CLASSIFICATION: 435
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APPLICANT: LOWE, JC
APPLICANT: LENNON,
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APPLICANT: Eric H. Holmes et al.
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAI GANGLICSIDE
TITLE OF INVENTION: GMI-SPECIFIC ALPHA1-2 FUCOSYLIFRANSFERASE AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: SANDRIN, MAURO S.
APPLICANT: MCKENRIE, IAN C. F.
TITLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
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                                                         301 TFGIWAAYLAGGDTIXLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK
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CURRENT APPLICATION NUMBER: US/09/298,886
CURRENT FILING DATE: 1999-04-26
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SLPVLHSSTASRVPWONYHLNDMMEERYRHIPAPYVRLTGYPCSWTFYHHLRHEILREFT 173
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PRIOR APPLICATION NUMBER: PCT/AU97/00540
PRIOR FILING DATE: 1997-08-22
PRIOR FILING DATE: 1997-08-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/09254077A Patent No. 6399758
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Best Local Similarity 57.69
Matches 209; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 PTSQRAPSRPLGGMWTINAMGRLGNQMGEYATLYALAKENGRPAYIPAQMHSTLAPIFRI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFT 180
                                                                                                                                                                                                                                                                                                                             61 RDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRI 120
                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                       Sequence 9, Application US/09254077A
Patent No. 6399758
GENERAL INFORMATION:
APPLICANT: SANDRIN, MAURO S.
APPLICANT: MCKENZIE, IAN C. F.
TITLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
FILE REFERENCE: 30562.50590
CURRENT APPLICATION NUMBER: US/09/254,077A
CURRENT FILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: PCT/AU97/00540
PRIOR PILING DATE: 1997-08-23
PRIOR PILING DATE: 1996-08-23
PRIOR PILING DATE: 1996-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230 WFRARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHIIMTI
                                                                                                                                                                                                                                1 MASAQVPFSFPLAHFLIFVFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMR
                                                                                                                                                                                                                                                                                                                                                                                      SLPVLHSDTAKKIPWQNYHLNDWMEERYRHI-PGHFVRFTGYPCSWTFYHHLRPEILKEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 MFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 347;
                                                                                                                                                   Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 72.5%; Score 1472.5; DB 4; Best Local Similarity 77.6%; Pred. No. 1.4e-161; Matches 274; Conservative 31; Mismatches 41;
                                                                                                                                                   72.6%; Score 1475; DB 4; 77.7%; Pred, No. 6.9e-162;
                                                                                                                                                                                          30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
                                                                                                                                                                        Best_Local Similarity 77.7%
Matches 275; Conservative
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver.
                                SEQ ID NO 11
LENGTH: 344
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Lepus Sp.
US-09-254-077A-9
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                                                                                                                 US-09-298-886-11
                                                                                                                                                     Query Match
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171 LRPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMFGVV 228 229 ADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFAL 288 289 LTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADL 348 LHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM 240 FRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIG 300 51 SGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEXATLFALARMNGRLAFIPASM 110 -----GIWTIHPDGRFGNQMGQYATLLALAQLNGRRAFILPAM 116 111 HNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHH 170 11 LAFLLVCALSAFSFLLHHUDLFRNGLALSLPCLERQPVPAPVAIVCLPVTSPASNASSC 70 GENERAL INFORMATION:
APPLICANT: SANDRIN, MADRO S.
APPLICANT: SANDRIN, MADRO S.
TITLE OF INVENTION: NUCLBIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
FILE REFERENCE: 30562.509W
CURRENT APPLICATION NUMBER: US/09/254,077A
CURRENT FILING DATE: 1999-06-11 174 LHDHVREEAQAFLRGLRVNGSRPSTFVGVHVRRGDYVRVMPQVWKGVVADRGYLEQALDW TFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 353 Length 373; DB 4; 53.5%; Score 1086.5; DB 4; 57.6%; Pred. No. 6.7e-117; iive 51; Mismatches 62;

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TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES, ON GLYCOPROTREINS,
TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE IS
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE
CORRESPONDENCE 14
CORRESPONDENCE ADDRESS:
ADDRESSE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 P-----QH-PASISGTWTVYPNGRFGNQMGQYATTLALAQLNGRRAFILPAMHAALAP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 PEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAP 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 LAFLLVCVLSVIFFLHIHQDSFPHGLGLSILCPDRRLVTPPVAIFCLPGTAMGPNASSSC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---RIVKLOPLSEKELPMTTOMSSGNTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 KEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYL
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                                                                                                                                                                                                                                                                                                                                                                            STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U$/08/393,246
FILING DATE: U$/08/393,246
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: U$ 08/220,433
FILING DATE: 30-MAR-1994
APPLICATION NUMBER: U$ 07/914,281
FILING DATE: 20-JUL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.0%; Score 1057.5; DB 1; 56.5%; Pred. No. 1.5e-113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                Sequence 6, Application US/08393246 Patent No. 5595900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                   JOHN B
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
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Best Local Similarity
Matches 205; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: LOWE,
         363 AKP 365
                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER:
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                  Sequence 6, Application US/07914281
Patent No. 5324663
GENERAL INFORMATION:
APPLICANT: LOWE, JOHN B.
TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
ITTLE OF INVENTION: GLYCOLIFPIS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURINGER OF SEQUENCES: 14
CORRESPONDENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 PEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAP 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 IFRISLPVLHSDIAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEIL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 KEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYL 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---RIVKLQPLSEKELPMTTQMSSGNTES 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 LAFLLVCVLSVIFFLHIHQDSFPHGLGLSILCPDRRLVTPPVAIFCLPGTAMGPNASSSC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 365;
                                                                                                                                                                                                                                           SEE: OBLON. SPIVAK, MCCLELLAND, MAIER & NEUSTADT, SEE: P.C. 1755 Jefferson Davis Highway, Fourth Floor Arlington Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version #1.25
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56.5%; Pred. No. 1.5e
live 46; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 530
ATTORNEYAGENT INFORMATION:
NAME: LAVAlleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2563-060-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PATENTIN RELEASE #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/914,281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J9920720
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
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Best Local Similarity
Matches 205; Conserv
                                                                                                                                                                                                                                                                                                                                                              U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                   22202
                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
US-07-914-281-6
                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                  CITY: A
STATE:
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Gaps

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ATTORNET AGENT INFORMATION:
NAME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2383-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08525058A Patent No. 5770420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.0%;
56.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 248855 OPAT UP
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-525-058A-6
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-525-058A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        363 AKP
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OTHER INFORMATION: /note= "GDP-L-fucose:beta-D-Galactoside-2-alpha-L-fucosyl PUBLICATION INFORMATION:
AUTHORS: Larsen, et al.
243 RQAMDWFRARHEAPVEVVTSNGMEWCKENIDTSQGDVTFAGDGQEATPWKDFALLTQCNH 302
                                                                      295 TIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLKA 354
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                                                                                                                                                                                                                                                                                         APPLICANT: Falk, Per APPLICANT: Gordon, Jeffrey I.
APPLICANT: Gordon, Jeffrey I.
TITLE OF INVENTION: Disease
TITLE OF INVENTION: Disease
CORRESPONDENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                    Street, Suite 2800
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Proc. Nat'l Acad. Sci.
                                                                                                                                                                                                                                        Sequence 1, Application US/08273411
Patent No. 5625124
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INPORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REPERENCE/DOCKET NUMBER: WUIO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 815-6508
TELEPAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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1100 Peachtree Stree
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COUNTRY: USA
ZIP: 30309-4530
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Matches 205;
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GENERAL INCOMMATION:
GENERAL INCOMMATION:
APPLICANT: LOWE, JOHN B.
TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES, AND FOR THE ISOLATION
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
57 PEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAP 116
                                                                                                                                                            117 IFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEIL 176
                                                                                                                                                                                                                   243 ROAMDWFRARHEAPVFVVTSNGMEWCKENIDTSQGDVTFAGDGGEATPWKDFALLTQCNH 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-----QH-PASLSGTWTVYPNGRFGNQMGQYATLLALAQLNGRRAFILPAMHAALAP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235 EKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNH 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295 TIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLKA 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1057.5; DB 1; Length 365; Pred. No. 1.5e-113;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,058A
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CLASSIFICATION:
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                Query Match
Best Local S:
Matches 2055
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Z-ALPHA-L-FUCOSYLTRANSFERASES, DNA SEQUENCES ENCODING THE
SAME, METHOD FOR PRODUCING THE SAME AND A METHOD OF
GENOTYPING A PERSON
    4;
                                                                                                     IFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEIL 176
                                                                                                                                                           PEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAP 116
                                                                                                                                                                                                    KEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYL 234
                                                                                                                                                                                                                                                          EKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNH 294
                                                                                                                                                                                                                                                                            TIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWYGIPADLSPLLKA 354
    Gaps
                           --RIVKLQPLSEKELPMTTQMSSGNTES 56
                                                     LAFILVCVLSVIFFLHIHQDSFPHGLGLSILCPDRRLVTPPVALFCLPGTAMGPNASSSC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON
 Indels
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SOFTWARE: PatentIn Release #1.0, Version #1.30
 87;
 Mismatches
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APPLICATION NUMBER: US/08/395,800A
FILING DATE: 28-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08395800A
Patent No. 5807732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 28-FEB-1995
CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-320
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 6;
46;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
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APPLICANT: GIORGI, DOMINIQUE
APPLICANT: KELLY, ROBERT J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GREGORY
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amino acid
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Conservative
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                           LAHFLIFVFVTSTIHLQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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: USA
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GENERAL INFORMATION:
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TOPOLOGY:
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205;
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Matches
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SEQUENCES ENCODING THE
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                                               Gaps
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                                               25;
  Length 365;
                                               87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDP-L-FUCOSE: BETA-D-GALACTOSIDE
Score 1057.5; DB 1;
Pred. No. 1.5e-113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patentin Release #1.0, Version #1.30
                                               46; Mismatches
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28-FEB-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: LOWE, JOHN B
APPLICANT: LOWE, JOHN B
APPLICANT: ENOUGHER, SYLVIE
APPLICANT: GLORE, SOMINIQUE
APPLICANT: KELY, ROBERT J
TILLE OF INVENTION: GDP-L-FUCOS
TITLE OF INVENTION: 2-ALPHA-L-F
TITLE OF INVENTION: GAME, METHO
TITLE OF INVENTION: GAME, METHO
TITLE OF INVENTION: GAME, METHO
TITLE OF INVENTION: GENOTYPING
NUMBER OF SECUENCES: 22
CORRESPONDENCE ADDRESS:
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TELEFAX: (703) 413-220
TELES: 248955 OPAT UR
INFORMATION FOR SEC ID NO: 10:
SEQUENCE CHARACTERISTICS:
52.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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amino acid
                                               Conservative
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FILING DATE: 28-FEE
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                   al Similarity
205; Conserv
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Score 1057.5; DB 1; Length 365; pred No 1 5e-113.
                                                                      52.0%;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-395-800A-10
                                                                      Query Match
Best Local Similarity
Matches 205; Conserv
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Gaps	ES 56 SC 70
25;	MSSGNT ::: GPNASS
Indels	SKELPMTTQ: FCLPGTAM
87;	-RIVKLOPLSEKE: : :: DRRLVTPPVAIFC:
Mismatches	RIVK : GLSILCPDRRLV
6, Pt 46;	SFPHGI
est boot similaring 30.3%; Fred. No. 1.35-113; atches 205; Conservative 46; Mismatches 87; Indels 25; Gaps	12 LAHFLIFVEVISTIIHLQQRIVKLQPLSEKELPMTIQMSSGNTES 56
205;	LAHFLI : LAFLLV
tches	12

⁵⁷ PEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAP 116 qq

QΥ

QYq QΥ

¹⁷⁷ KEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYL 234

Вþ

QΥ QQ

³⁵⁵ LTP 357

³⁶³ AKP 365

Search completed: May 27, 2003, 15:11:50 Job time: 17.6237 secs

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Sequence 11, Appl
Sequence 11, Appl
Sequence 10, Appl
Sequence 6, Appli
Sequence 4, Appli
Sequence 13, Appli
Sequence 13, Appli
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Sequence 2, A
Sequence 25,
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| cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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| cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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Compugen Ltd.
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US-10-214-524-25
US-09-479-614-29
US-09-764-868-647
US-09-815-379-10
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US-09-051-034A-4
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GenCore version
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Listing first 45 summaries
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ALIGNMENTS

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                                                                  GENERAL INFORMATION:
APPLICANT: Eric H. Holmes et al.
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAT GANGLIGSIDE
TITLE OF INVENTION: GMI-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENTION: THEREOF
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100.0%; Pred. No. 1.6e-200;
Live 0; Mismatches 0;
                                                                                                                                                         FILE REFERENCE: 8511-029
CURRENT APPLICATION NUMBER: US/09/999,672
CURRENT FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: US/09/298,886
PRIOR FILING DATE: 1999-04-26
                                     Sequence 8, Application US/09999672 Patent No. US20020127655A1
                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Rattus norvegicus US-09-999-672-8
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SOFTWARE: Patentin Ver. 2.
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                            241 FRARYSSPVFVVISNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIG 300
                                                                             TFGIWAAYLAGGDIIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLKALTPACP 360
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APPLICANT: Eric H. Holmes et al.
APPLICANT: Eric H. Holmes et al.
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE
TITLE OF INVENTION: GMI-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 811-029
CURRENT APPLICATION NUMBER: US/10/040,863
CURRENT APPLICATION NUMBER: 09/298,886
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID MOS: 29
SOFTWARE: PATENTIN VEY: 2.0
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                                                                                                                                                                                                                             ; Sequence 8, Application US/10040863; Patent No. US20020137165A1
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US-09-999-672-10
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Sequence 10, Application US/09999572 Patent No. US20020127655A1 GENERAL INFORMATION:

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APPLICANT: Eric H. Holmes et al.

TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAI GANGLIOSIDE
TITLE OF INVENTION: GAL-SPECIFIC ALPHA1-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: 8511-029
CURRENT APPLICATION NUMBER: US/09/999,672
CURRENT APPLICATION NUMBER: US/09/298,886
PRIOR APPLICATION NUMBER: US/09/298,886
PRIOR FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
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Patent No. US20020137165a1
GENERAL INFORMATION:
APPLICANT: Eric H. Holmes et al.
TILLE OF INVENTION: MUCLEIC ACIDS AND PROTEINS OF A RAT GANGLICSIDE
TILLE OF INVENTION: GMI-SPECIFIC ALPHA1-2 FUCOSYLFRANSFERASE AND USES
TILLE OF INVENTION: THEREOF
FILE REPERENCE: 8511-029
CURRENT APPLICATION NUMBER: US/10/040,863
CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: 09/228,886
PRIOR FILING DATE: 1999-04-23
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Pred. No. 1.4e-186;
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93.3%; Score 1896; DB 12;
Best Local Similarity 100.0%; Pred. No. 1.4e-1866;
Matches 353; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                      93.3%; Scor.
v 100.0%; Pred. No. 1...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Rattus norvegicus
US-09-999-672-10
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US-10-040-863-10
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LENGTH: 353
TYPE: PRT
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Best Local 9
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US-09-999-672-11
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                                                                             GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120
                                                                                                                                  147
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GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER
                                                                                                               YRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHYRBEAQAFLRGLRVNGSQPSTFV
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Pred. No. 4.5e-146;
; Mismatches 30;
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APPLICANT: SANDRIN, MAURO SERGIO
TITLE OF INVENTION: IMPROVED NUCLEIC ACIDS ENC
TITLE OF INVENTION: GLACOSYLTRANSFERASE
FILE REFERENCE: 30562.603WO
CURRENT APPLICATION NUMBER: U$/09/051,034A
CURRENT APPLICATION NUMBER: PCY/AU97/00492
PRIOR FILING DATE: 1997-08-01
PRIOR FILING DATE: 1996-08-21
PRIOR APPLICATION NUMBER: 60/024,279
PRIOR FILING DATE: 1996-08-21
PRIOR PRILING DATE: 1996-08-21
PRIOR FILING DATE: 1996-08-21
PRIOR FILING DATE: 1996-08-21
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US-09-051-034A-2
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LENGTH: 340
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Best Local 3
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                                                                                                                                                                                                 Sequence 11, Application US/0999672

Sequence 11, Application US/0999672

GENERAL INFORMATION:
APPLICANT: Eric H. Holmes et al.
APPLICANT: Eric H. Holmes et al.
TITLE OF INVENTION: UNCLEIC ACIDS AND PROTEINS OF A RAT GANGLICSIDE
TITLE OF INVENTION: THEROE TITLE OF INVENTION: THEROE TITLE OF INVENTION: US/09/999,672

CURRENT APPLICATION NUMBER: US/09/999,672

CURRENT FILING DATE: 2001-10-31
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12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: US/09/298,886
PRIOR FILING DATE: 1999-04-26
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PRIOR APPLICATION NOMBER: 09/298,886
PRIOR FILING DATE: 1999-04-23
SUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
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Patent No. US20020137165A1
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SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 29
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us-10-040-863-8.rapb

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123 VFRITLPVLAPEVDSRIPWRELQLHDWMSEEYADLRDPFLKLSGFPCSWTFFHHLREGIR 182
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                                                                                                                                                        235 EKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55
TELECOMMUNICATION INPORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
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CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/09863475A Patent No. US20020102688A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 20-JUL-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (703)521-4500
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TELEX: 248855 OPAT UR
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Best Local Similarity 56.58
Matches 205; Conservative
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APPLICANT: Clark, A. John
APPLICANT: Clark, A. John
APPLICANT: Clark, A. John
TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Compatible for Human
TITLE OF INVENTION: Recombination and a Carbohydrate Determinant Selection System
FILE REFERENCE: 731/002
CURRENT APPLICATION NUMBER: US/10/105,963
CURRENT FILING DATE: 2002-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                       71 P-----QH-PASLSGTWTVZPNGRFGNQMGQYATLLALAQLNGRRAFILPAMHAALAP 122
                                                                                                                                                                                                                                                                                                        61 RDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRI 120
                                                                                                                                                                                                                                                                                                                                                                                            SLPVLHSDTAKKIPWQNYHLNDWMEERYRHI-PGHFVRFTGYPCSWTFYHHLRPEILKEF 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 PEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAP 116
                                                                                                                                                                                                                                               11 LAFLLVCVLSVIFFLHIHQDSFPHGLGLSILCPDRRLVTPPVAIFCLPGTAMGPNASSSC 70
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                                                                                                                                 Length 344;
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                                                                                                                               72.6%; Score 1475; DB 12; 77.7%; Pred. No. 2.7e-143;
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                                                                                                                                                                        30; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/10105963
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NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
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GENERAL INFORMATION:
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                                                                                                                                                                        Matches 275; Conservative
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                                         TYPE: PRT
ORGANISM: Homo sapiens
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US-10-105-963-10
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US-10-105-963-10
                                                                                    US-10-040-863-11
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SEQ ID NO 11
LENGTH: 344
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APPLICANT: LOWE, JOHN B.

TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
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                                                                                                                                                                                                                                                                                                               STREET: 1755 Jefferson Davis Highway, Fourth Floor
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PAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEW
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Patent No. US20020129395A1
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SOFTWARE: Patentin Ver, 2
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Best Local Similarity
Matches 194; Conserv
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APPLICANT: BOSWORTH,
APPLICANT: VOGELI, I
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ORGANISM: Porcine
                                                                                 VGIPADLSPL
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US-09-844-268-13
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                                                                                                          117 IFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEIL 176
                                                                                                                                           123 VFRITLEVLAPEVDSRTPWRELQLHDWMSEEYADLRDFLKLSGFPCSWTFFHHLREQIR 182
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             70
PEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAP
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APPLICANT: MCKENZIE, IAN FARQUHAR CAMPBELL
APPLICANT: SANDRIN, MANDO SERGO
TITLE OF INVENTION: IMPROVED NUCLEIC ACIDS ENCODING A CHIMERIC
TITLE OF INVENTION: GLYCOSLITRANSFERASE
TITLE OF INVENTION: GLYCOSLITRANSFERASE
CURRENT APPLICATION NUMBER: 05/09/051,034A
CURRENT FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: PCT/AU97/00492
PRIOR APPLICATION NUMBER: PCT/AU97/00492
PRIOR PILING DATE: 1998-001
PRIOR FILING DATE: 1998-001
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1996-08-02
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PRIOR FILING DATE: 1996-08-21
NIMBER ON THE PO14
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Best Local Similarity 62.6%;
Matches 194; Conservative 3
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                                                                                                                                                                                                                                                                                                                                                                               355 LTP 357
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LENGIH: 365
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Patent No. US20020133836A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BOSWORTH, BEAD
APPLICANT: VOGELI, PETER
TITLE OF INVENTION: METHODS AND COMPOSITIONS TO IDENTIFY SWINE GENETICALLY
TITLE OF INVENTION: RESISTANT TO F18 E. COLI ASSOCȚATED DISEASES
FILE REFERENCE: 21419/9903844,705
CURRENT APPLICATION NUMBER: US/09/844,705
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: VOGELI, PETER
TITLE OF INVENTION: METHODS AND COMPOSITIONS TO IDENTIFY SWINE GENETICALLY
TITLE OF INVENTION: RESISTANT TO FIRE E. COLI ASSOCIATED DISEASES
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                                 44 PMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRL 103
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62.6%; Pred, No. 5.8e-99;
Hive 38: Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 21419/90366
CURRENT APPLICATION NUMBER: US/09/844,268
CURRENT FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: 09/443,766
PRIOR FILING DATE: 1999-11-19
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CURRENT APPLICATION NUMBER: US/09/479,614
CURRENT FILING DATE: 2000-01-07
EARLIER APPLICATION NUMBER: 60/115,033
EARLIER FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                          RESULT 14
US-09-479-614-14
'Sequence 14, Application US/09479614
'Publication No. US20030013183A1
'GENERAL INFORMATION:
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Best Local Similarity 20.69
Matches 89; Conservative
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ORGANISM: Felis catus
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US-09-479-614-14
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                                                                                                                                                                                                                                                                                                    44 PMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRL 103
                                                                                                                                                                                                                                                 51 PVAIFCLAGTPVHPNASDSCPKH-PASFSGTWTIYPDGRFGNQMGQYATLLALAQLNGRQ 109
                                                                                                                                                                                                                                                                                104 AFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221
                                                                                                                                                                                                                                                                                                                                                                                                                     281
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                                                                                                                                                                                              3; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----TLFALARMNGRLAFIPASMHNALAPIFRIS-- 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                SWIFYHHLRPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMP
                                                                                                                                                                                                                                                                                                                                                                222 NVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGS
                                                                                                                                                               Length 365;
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                                                                                                                                                               DB 10;
                                                                                                                                                        51.4%; Score 1044.5; DB 10.
62.6%; Pred. No. 5.8e-99;
tive 38; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
6.9%; Score 141; DB 10;
Best Local Similarity 24.0%; Pred. No. 3.8e-06;
Matches 81; Conservative 33; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Taylor, Diane
APPLICANT: Wang, Ge
APPLICANT: Palcic, Monica
TITLE OF INVENTION: ALPHA 1,2-FUCOSYLTRANSFERASE
FILE REFERENCE: 07254-061002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/848,838
CURRENT FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: US 09/433,598
PRIOR FILING DATE: 1999-11-02
PRIOR APPLICATION NUMBER: US 60/107,268
PRIOR APPLICATION NUMBER: US 60/107,268
PRIOR APPLICATION NUMBER: US 60/107,268
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FASTERO for Windows Version 4.0
PRIOR APPLICATION NUMBER: 09/443,766
PRIOR FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09848838 Patent No. US20020037570A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Helicobacter pylori
US-09-848-838-2
                                            SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 365
                                                                                                                                                                       Best Local Similaria,
Matches 194; Conservative
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                                                                                          TYPE: PRT
CRGANISM: Porcine
US-09-844-705-13
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US-09-848-838-2
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LENGTH: 300
                                                                                                                                                          Query Match
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APPLICANT: Weber, Eric
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
FILE REFERENCE: P-1047
70 QHLPKLVRDALKYIGFDRVSQEIVFEXEPKLLKPSRLTYFFGYFQDPRYFDAISSLIKQT 129
                                               179 FTL------HDHVREBAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMFRGVVA 229
                                                                                                                                                                                                                                                                        226 DKEEEAYWDMLLMQSCKHGIIANSTYSWWAAYL------MEN---PEKIIIGFKHWLFG 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 ASIQAPLVFPLATCCKGTIATAPSVTLGCLVTGYFPMPVTVTWDARSLNKSVV----- 56
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                                                                                                                                            230 DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFA--.
                                                                                                                                                                                          ------SPFLKVFK
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40; Mismatches 127; Indels 176;
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                                                                                                                                                                                                                                                                                                                                         333 PEAAFLPEWVGIPADLSPLLKALTPACPRSHFHLKAK 369
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122 -TEPATLOETSGLYTTTSHVTVSGEWAKQKFTCSVAHAESPTINKTVSACTMNFIPPTVK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229 ADRGYLEKALDMFRARYSSPVFVVTSNGM--AWCRENINASRGDVVFAGNGIEGSPAKDF 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----HFLIFVFVTSTIIHLQQRIVKLQPLSE 40
                                                                                                                                                                                                                                                                                                                                                                                                                                41 KELPMTTQMSSG------65
                                                                                                                                                                                                                                                                                                       Query Match
5.6%; Score 113; DB 9; Length 496;
Best Local Similarity 20.6%; Pred. No. 0.0061;
Matches 89; Conservative 40; Mismatches 127; Indels 176;
                                                                                                                                                                                                                                                                                                                                                                      2 ASAQVPFSFPLA-----
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                                                                                                                                                                                                                                                            ; ORGANISM: Felis catus US-09-479-614-2
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Search completed: May 27, 2003, 15:25:41 Job time : 19.4181 secs

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2652.940 Million cell updates/sec
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               283224 seqs, 96134422 residues
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                                                                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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ALIGNMENTS

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RESULT 1 A5608 alpha(1.2)fucosyltransferase Sec2, long form - human clapha(1.2)fucosyltransferase Sec2, long form - human clapha(1.2)fucosyltransferase Sec2, long form - human clapses Homo Saptens (man) C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995; Recally, R.J.; Rouquier, S.; Glorgi, D.; Lennon, G.(J. Biol. Chem. 270, 4640-4649, 1995 A;Title: Sequence and expression of a candidate for the with the non-Secretor phenotype. A;Reference number: A56098; MUID:95181460; PMID:7874 A;Accession: A56098 A;Accession: A56098 A;Residues: 1-343 <
Aducties Oy 1 Db 1
Qy 61 Db 50
Oy 121 Db 110
Qy 181 Db 170
Qy 241 Db 230
Qy 301 Db 290

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C,Accession: A36647
R;Larsen, R.D.; Ernst, L.K.; Nair, R.P.; Lowe, J.B.
R;Larsen, R.D.; Ernst, L.K.; Nair, R.P.; Lowe, J.B.
A;Title: Molecular cloning, sequence, and expression of a human GDP-L-fucose:beta-D-g
A;Reference number: A36047; MUID:90370848; PMID:2118655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.5pecies: Homo sapiens (man)
C:Species: 16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change 10-Sep-1997
                                                   A;Cross-references: GB:M35531; NID:9183887; PID:9306830
C;Keywords: 91ycosyltransferase; hexosyltransferase; transmembrane protein
          HNALAPIFRISLPVLASDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHH 170
                                                                                                                                                                                                                                                                         229 ADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFAL 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 LAFLLVCVLSVIFFLHIHQDSFPHGLGLSILCPDRRLVTPPVAIFCLPGTAMGPNASSSC 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 RQAMDWFRARHEAPVFVVTSNGMEWCKENIDTSQGDVTFAGDGQEATPWKDFALLTQCNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.0%; Score 1057.5; DB 2; Length 365; lilarity 56.5%; Pred. No. 1.5e-80; Conservative 46; Mismatches 87; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             galactoside 2-alpha-L-fucosyltransferase (EC 2.4.1.69) - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 LAHFLIFVFVTSTIIHLQQ-----
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-365 < LAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         349 SPL 351
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                    C. Species: Oryctolagus cuniculus (domestic rabbit)
C. Species: Oryctolagus cuniculus (domestic rabbit)
C. Species: Oryctolagus cuniculus (domestic rabbit)
C. Accession: B5632
C. Accession: B5632
C. Accession: B5632
C. Atitle: Molecular cloning and expression of two types of rabbit beta-galactoside alphal Article: Molecular cloning and expression of two types of rabbit beta-galactoside alphal Article: Molecular cloning and expression of two types of rabbit beta-galactoside alphal Article: Molecular cloning and expression of two types of rabbit beta-galactoside alphal Arcession: B5632: MUID:95238380; PMID:7721792
A. Status: preliminary
A. Molecular type: mRNA
A. Residues: 1-354 < HIT>
A. Cross-references: GB:X80225; NID:9854356; PIDN:CAA56512.1; PID:9854357
C. Keywords: transmembrane protein
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 05-Nov-1999
C;Accession: A56392
R;Hitoshi, S.; Kusunoki, S.; Kanazawa, I.; Tsuji, S.
A;Hitoshi, S.; Kusunoki, S.; Kanazawa, I.; Tsuji, S.
A;Hitoshi, S.; Kusunoki, S.; Kanazawa, I.; Tsuji, S.
A;Hitoshi, S.; Kusunoki, S.; Kusunoki, S.; Kanazawa, I.; Tsuji, S.
A;Hitoshi, S.; Kusunoki, S.; Kanazawa, I.; Tsuji, S.
A;Hitoshi, S.; Kusunoki, S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PWQNYHLNDWMEERYRHIPVPYVRLTGYPCSWTFYHHLIHEILREFTLHDHYREEAQAFL 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 HFLIFVFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRG 73
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A)Status: preliminary
A)Andlecule type: mRNA
A)Residues: 1-373 <HITT>
A)Cross-references: GB:X80226; NID:g854354; PIDN:CAA56513.1; PID:g854355
C)Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 MFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 354;
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beta-galactoside alphal, 2-fucosyltransferase II - rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.9%; Score 1319.5; DB 2; 73.2%; Pred, No. 1.9e-102; live 27; Mismatches 47; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.5%; Score 1086.5; DB 2; 57.6%; Pred. No. 5.7e-83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              314 TIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLL 352
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Best Local Similarity
Matches 248; Conserv
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Best Local Similarity
Matches 209; Conserv
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hypothetical protein wblA [imported] - Vibrio cholerae
C;Species: Vibrio cholerae
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 28-Jul-2000
C;Accession: T44228
R;Yamasaki, S.; Shimizu, T.; Hoshino, K.; Ho, S.T.; Shimada, T.; Nair, G.B.; Takeda,
Gene 237, 31-332, 1999
A;Title: The genes responsible for O-antigen synthesis of Vibrio cholerae Oi39 are cl
A;Reference number: Z22749; MUID:99453293; PMID:10521656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rinnorwhous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A.Title: Genome sequence of the nematode C. elegans: a platform for investigating bio A.Title: Genome sequence of the nematode C. elegans: a platform for investigating bio A.Title: Genome sequence of the nematode C. elegans: a platform for investigating bio A.Note: see websites genome wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_A.Accession: H87911
A.Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
A.Kocession: H87911
A.Status: preliminary
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-443 <STO>
A.Cross-references: GB:chr_I; PIDN:AAC16988.1; PID:g3150470; GSPDB:GN00019; CESP:B020
A.Genetics:
A.Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A)Residues: 1-281 <ram>
A)Cross-references: EMBL.AB012957; NID:g4115688; PIDN:BAA33632.1; PID:g3721682
A)Experimental source: strain 022
C;Genetics:
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C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: H87911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----NDWMEERYRHI------PGHFVRFT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 GYPCSWIFYHHLRPBILKEFTLHDHVRBEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHV 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  220 MPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIE 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  280 GSPAKDFALLTQCNHTIMTIGTFGIWAAYL-AGGDTIYLANYT------LPDS 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---IDDLMLMCQCQHNIVANSSFSWWAAWLNSNVDKIVIAPKTWAAENPKGYKWVPDS 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: wbla
C;Superfamily: Vibrio cholerae hypothetical protein wbla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.6%; Score 214.5; DB 2; 26.5%; Pred. No. 2.5e-10; Live 50; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 183; DB 2;
Pred. No. 1.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
9.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 DTAKKIPWQNYHL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Simi
Matches 79;
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                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223
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   galactoside 2-alpha-L-fucosyltransferase (EC 2.4.1.69) B - rat (fragment)
N;Alternate names: alpha-1,2-fucosyltransferase
C;Species: Rattus norvegicus (Norway rat)
C;Dactes: Sattus 54649
R;Piau, J.P.; Labarriere, N.; Dabouis, G.; Denis, M.G.
B;Piau, J.P.; Labarriere, N.; Dabouis, G.; Denis, M.G.
A;Title: Evidence for two distinct alpha-(1,2)-fucosyltransferase genes differentially A;Reference number: S46494
A;Accession: S46494
A;Accession: S46494
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A)Molecule type: mRNA
A)Molecule type: mSNA

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C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-May.1995 #sequence_revision 17-Nov-1995 #text_change 08-Oct-1999
C:Accession: S51882; S46493
                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-159 <PIA>
A; Cross-references: EMBE:L26010; NID:g414816; PIDN:AAB41515.1; PID:g414817
G; Genetics:
A; Gene: FTB
C; Keywords: glycosyltransferase, hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222 NVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGS 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220 MPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIE 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                282 PAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 PAKDFALLTQCNHTIMITGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 159;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 846; DB 2; Length 15
Pred. No. 2.3e-63;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    342 VGIPADLSPLLKALTPACPRSHFHLKAKGVTCYVAGRAF 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 581; DB 2;
Pred. No. 2.6e-41;
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A, Molecule type: mRMA
A, Molecule type: mRMA
A, Cross-references: EMBL:126009
C, Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R.Piau, J.P.; Labarriere, N.; Dabouis, G.; Denis, submitted to the EMBL Data Library, November 1993 A;Reference number: S51582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
28.6%; Score 581; DB
Best Local Similarity 73,2%; Pred. No. 2.6e
Matches 104; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                280 GSPAKDFALLTQCNHTIMTIGT 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 99.4
Matches 158; Conservative
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334 EFISEDXYLPHW 345

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A) Cross-references: EMBL: AF016654; PIDN: AAB66030.1; GSPDB:GN00020; CESP:C17A2.4
A) Experimental source: strain Bristol N2; clone C17A2
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A.Status: preliminary: translated from GB/EMBL/DDBJ
A.Status: preliminary: translated from GB/EMBL/DDBJ
A.Status: preliminary: translated from GB/EMBL/DDBJ
A.Status: 1.335 < CANV>
A.Status: 1.335 < CANV>
A.Cross-references: EMBL:AF024500; PIDN:AAB70365.1; GSPDB:GN00023; CESP:K06H6.6
C.Genetics: Strain Bristol N2; clone K06H6.6
A.Gene: CESP:K06H6.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
Aypothetical protein C17A2.4 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 29-0ct-1999 #sequence_revision 29-0ct-1999 #text_change 21-Jul-2000
C.Accession: T31916
B.Sammons, L.; Wohldmann, P.
Submitted to the BREL Data Library, July 1997
A.Description: The sequence of C. elegans cosmid C17A2.
A.Reference number: 221098
A.Accession: T31916
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Status: A.SAM>
A.STATUS: A.STATUS: A.SAM>
A.STATUS: A.SAM>
A.STATUS: A.STATUS: A.SAM>
A.STATUS: A.STATUS: A.STATUS: A.SAM>
A.STATUS: A.STATUS: A.SAM>
A.STATUS: A.STATU
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C:Species: Caenorhabditis elegans
C:Date: 29-Oct.1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 LRGMFTINSIGRLGNQMGEYATLFALARMNGR--LAFIPASMHNALAPIFRISLP---- 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 RPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDXVHVMPNVWKGV-VAD 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 --VLHSDTAKKI---PWQ----NYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231 RGYLEKALDMFRARYSSPV-----FVVTSNGMAWCR---EN--INASRGDVVFAGNG 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 PDFIRNSVKYIAENFIPEIEYKKVHRKVVIFGDDLEFMRSLFENSVVSTDEPEYMFPASY 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 LAHFLIF-VFVTSTIIHLQQRIVKLQPLSEKELPWTTQMSSGNTESPEMRRDSEQHGNGE 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38 ------SRLGNHIFFFASLFGLSERLHRTPLFLVENEFHQKMLDETRKVMPGLVEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 2
A;Introns: 94/3; 133/3; 168/2; 272/1
C;Superfamily: Caenorhabditis elegans hypothetical protein C14C6.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.7%; Score 156.5; DB 2; Length 348; 20.9%; Pred. No. 2.3e-05; tive 57; Mismatches 118; Indels 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      278 I--EGSPAKDFALLTQ-CNHTIMTI--GTFGIWAAYLAGGDTIY 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 YISQNSPAEDLIYSKQNCDIVLISAPKSTFGWWIGYFSKGNKVF 291
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R; David, M.; Wohldmann, P.; Bauer, C.; Clarke, K.
submitted to the EMBL Data Library, September 1997
A; Reference number: 221147
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A;Gene: CESP:C17A2.4
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OY 223 VWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCI DD 226 RPSDATFTRAATDFLVDLYRKSHERVNVVVLGN OY 283 AKDFALLTQ DD 272 AHFTELQKPVNNSYDSSLPQISPSYTAILTPTLTPEIDI OY 305 WAAVLAGGD-TIYLANYTLEDSPPLKVFKPEAAFLPEWT DD 332 WLSYLAKRTATTYYRDILESKDGVAGEMHPEDFYPPEWT	RESULT 13 T22068 hypothetical protein F41D3.5 - Caenorhabditis ele C:Species: Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Date: 15-Oct-1999 #sequence_revision 15-Oct-199 C:Accession: T22068 R:White, S. submitted to the EMBL Data Library, November 1996 A:Reference number: 219508 A:Accession: T22068 A:Accession: T22068 A:Accession: T2006 A:	Query Match Best Local Similarity 23.4%; pred: No. 0.00 Matches 74; Conservative 48; Mismatches Qy 74 MFTINSIGRIGNOMGERATLFALARMNGRLAFIPASMH Db 49 MTTIVYGGIGNOMEPVISLIGIARKIRHALVFF QY 120ISLPVLHSDTAKKIPWQNYHLNDWMEE Db 104 EQVISVPIESETTEFAISSDCCRFELSDHIADES QY 169 HHLRPEILKEFTLHDHVREEAQAFIRGLRVNGSQPSTF Db 156 ADMKLSI-KEWLKPEDPEKFRMMISKTESQRHK QY 225 KGVVADRGYLEKALDMFRARYSSPVFVVISNGMAMCRE Db 204AGTDSNYTISAIDHLRSLYHGVIFIM-SNDPKWVKV	OY 285 DFALLTOCNHTIMII-GIFGIW :
A; Map position: 5 A; Introns: 17/1; 32/2; 58/1; 111/3; 150/3; 184/2; 218/1; 243/3; 272/1; 303/3 C; Superfamily: Caenorhabditis elegans hypothetical protein C14C6.3 Query Match 7: 6%; Score 153.5; DB 2; Length 335; Best Local Similarity 22.8%; Pred. No. 3.9e-05; Matches 77; Conservative 50; Mismatches 118; Indels 93; Gaps 19; Qy 51 SGWTESPEMRRDSECHGNGELRGMETINSIGRLGNOMGEYATLFALARANGRIAFIPA 108	### SETYRMIESSKEAIPGLVGQFEILNGKVPLYIKNTKLNTRCCVFVDPLIHBHNNDE 148 YRHIPGHFVRFGYPCSWIFYHHLRPEILKEFTLHDHVREBAQAFLRGLRVNGSQP 141 YLHLGRFYQAWKYPPSMRNELI	T20572 hypothetical protein F08A8.5 - Caenorhabditis elegans C; Bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000 C; Accession: T20572 R; Harris, B. S; Marris, B.	Query Match Best Local Similarity 21.4%; Score 146; DB 2; Length 383; Best Local Similarity 21.4%; Pred. No. 0.0002; Matches 87; Conservative 55; Mismatches 148; Indels 116; Gaps 16; Qy 13 AHFLIFVYTSTIHLQQRIVKLQPISEKELPMITQWSSGNTESPEMREDSEQHGNGELR 72 1 1 1 1 1 1 1 1 1

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L., Brown, E.D., Doig, P.C., Smith, D.
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| WIGYLSKNQSAVYYRDIRETKDQ 308
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FNSSDPVLQSNLEFLNQKLPRIS 103
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|-TCVHVRRGDFLTDEQH----- 203
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-----DIHFAYTVFEDRV 271
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|DLAFSRLFCDVTLITAPSSTFGW 331
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1012;
105; Indels 89; Gaps
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EWIKLKTDLN 377
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A; Title: Genomic sequence A; Reference number: A718 A; Accession: H71976	A; Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A; Reference number: A71800; MUID:99120557; PMID:9923682 A; Accession: H71976 A; Accession: H71976	Q G	181 LHDHVREEAQA : :	AQA : AET
type: DNX 1-299 <2 erences: tal sourc	ARN> GB:AE001447; GB:AE001439; NID:g4154583; PIDN:AAD05659.1; PID:g415458 ce: strain J99	oy Ob		Y SS
C;Genetics: A;Gene: jhp0086 C;Superfamily: Vibrio ch	cholerae hypothetical protein wblA	δλ		GIE
Ouery Match 6.6 Best Local Similarity 22:5 Matches 76; Conservative	6.6%; Score 133.5; DB 2; Length 299; 22.9%; Pred. No. 0.0016; ative 38; Mismatches 129; Indels 89; Gaps 13;	Db Sear	Db 305 YSVILPQN Search completed: May	 Мау
QY 81 GRLGNQMGEYA 	81 GRLGNOMGEYATLFALARWIGRLAFIPASMHNALAPIFRIS 121	Job	time : 28.77 se	ecs
Qy 122 :-LPVLHSDTAKKI 	22 :-LPVLHSDTAKKIPWQNYHLNDWMEERYRHI-PGHFVRFTGYPCSWTFYHHLRPEILKE 178			
QY 179 FTLHDHVRE : :: Db 130 FTLPPPPENGNNKK	FTLHDHVREEAQAFLRGLR-VNGSQPSTFVGVHVRRGDXVHVMPNVWKGVVADRG 232			
QY 233 YLEKALDMFRARYSSPVFVVTSNG : :: : Db 182 YQKKAVEYMAKRVPNMELFV	XLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFA 287 :			
OY 288LLTQCN Db 228 EEAYWDMLLMQSCK	LLTQCNHTIMFIGTFGIWAAYLAGGDTIXLANYTLPDSPFLKVFKPEAAF 337			
QY 338 LPEWVGIPADLSPL 280 CKEWVKI	LPEWVGIPADLSPLKALTPACPRSHFHLKAK 369			
RESULT 15				
725309 hypothetical protein T26 C;Species: Caenorhabditi C;Date: 15-0ct-1999 #seq C:Accession: T25309	125309 Nypothetical protein T26E4.4 - Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000 C.Accession: T25309			
R; McMurray, A. submitted to the EMBL Data Library, A; Exercise number: 220013	ata Library, October 1996 .			
A; Accession: 125309 A; Status: preliminary; translated A; Molecule type: DNA	translated from GB/EMBL/DDBJ			
A/Residues: 17303 CWIL) A/Cross-references: EMBL A/Experimental source: C	A: Gross references: EMBL: 281132; PIDN:CAB03434.1; GSPDB:GN00023; CESP:T26E4.4 A: Experimental source: clone T26E4			
C;Genetics: A;Gene. CESP:T26E4.4 A;Map position: 5 A;Introns: 50/1; 80/2; 140/3; C;Superfamily: Caenorhabditis	140/3; 179/3; 218/2; 253/1; 278/1; 306/3; 325/1; 342/3 bditis elegans hypothetical protein C14C6.3		r	
Query Match Best Local Similarity 20.7 Matches 61, Conservative	6.4%; Score 131; DB 2; Length 365; 20.7%; Pred. No. 0.0033; vative 43; Mismatches 106; Indels 84; Gaps 13;			
QY 84 GNQMGEYATLFALARMNGRLAFIPA 	GNOMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQ 136 : : :			
OY 137 NYHLNDWME D 143 SVSSHQMNWVKCCI	NYHINDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFT 180			

Qy	181	181 LHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEK 236	
qq	197	197 PSKMAKLAAETVLTSELKEDLIICTHIRRGDFQTDGVH-QPSDPNFTRA 244	
Ω.	237	237 ALDMFRARYSSPVFVVTSNGMAWCRENI	
QQ	245	245 ATDFLVKHYQKWHYRTTVVVFGNDVNFSKAVFEDRVSNSSVIPNRTTPPLNFPIPENSPK 304	
QΣ	269	269 GDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYIL 322	
Db	305	305 YSVILPQNSTPENDLAFSRQAPSSTFGWMLSYLAKRSAVYLRPFCL 350	

earch completed: May 27, 2003, 15:08:15

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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 27, 2003, 14:53:11; Search time 11.122 Seconds (without alignments) 1417.108 Million cell updates/sec

US-10-040-863-8 2032 1 MASAQVPFSFPLAHFLIFVF.....RSHFHLKAKGVTCYVAGRAF 380

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Total number of hits satisfying chosen parameters: 112892 seqs, 41476328 residues Searched:

112892

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% ' Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 FUT2_PIG STANDARD; PRT; 340 AA.	DT 15-UDN-2002 (Nel. 41, Last Sequence update) DE Galactoside 2-L-fucosyltransferase 2 (FC 2.4.1,69) (GDP-L-fucose:beta-	FUT2. Sus scrofa (Pig).	Mobil_TaxID=9823;		KA Meljerink E., Fries R., Voegeli P., Masabanda J., Wigger G., RA Stricker C., Neuenschwander S., Bertschinger H.U., Stranzinger G.:		RL Mamm. Genome 8:736-741(1997). pm (2))	[3]	RP SEQUENCE OF 69-334 FROM N.A.		RN [4] RP SEGUENCE OF 69-80: 119-133 AND 316-334	TISSUE=Submaxillary gland;	RT "Porcine submaxillary gland GDP-L-fucose: beta-D-qalactoside	RT alpha-2-L-fucosyltransferase is likely a counterpart of the human RT Secretor gene-appeded blood group transferance.	J	!	1 1		CC Inis SWISS-PROT entry is copyright. It is produced through a collaboration CC between the Swiss Institute of Bioinformatics and the EMBL outstation -	to the biropean Bioinformatics Institute. There are no restrictions on its case by non-profit institutions as long as its/content is in no way	CC entities requires a license agreement (See http://www.isb-sib.ch/announce/	or send an emair
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01-0CT-1996 (Rel. 34, Last sequence update)
15-JWA-2002 (Rel. 41, Last annotation update)
15-JWA-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 2 (EC 2.4.1.69) (GDP-L-fucose:beta-
D-galactoside 2-alpha-L-fucosyltransferase 2) (Alpha(1,2)FT 2)
(Fucosyltransferase 2) (Secretor blood group alpha-2-
fucosyltransferase) (Secretor factor) (Se) (SE2).
                                                                                                                                                                    SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 -----SSPQIKGMWIINAIGRLGNQMGEYATLYALARMNGRPAFIPPEMHSTLAPIFRI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 LHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 FRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MASAQVPFSFPLAHFLIFVFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95181460; PubMed=7876235; Kelly R.J., Rouguler S., Giorgi D., Lennon G.G., Lowe J.B.; Kelly R.J., Rouguler S., Giorgi D., Lennon G.G., Lowe J.B.; Sequence and expression of a candidate for the human Secretor blood group alpha(1,2)fucosyltransferase gene (FUT2). Homozygosity for an enzyme-inactivating nonsense mutation commonly correlates with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 SLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 LHNHVREBAQDFLRGLRVNGSRPSTYVGVHVRRGDYVHVMPNVWKGVVADRRYLEQALDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                          LUMENAL, CATALYTIC (POTENTIAL).

N-LINKED (GLCNAC. ) (POTENTIAL).

N-LINKED (GLCNAC. ) (POTENTIAL).

N-LINKED (GLCNAC. ) (POTENTIAL).

N-LINKED (GLCNAC. ) (POTENTIAL).
              EMBL, 070881, AAD81883.1, -.
EMBL, AF027304; AAC09170.1, -.
EMBL, AF027304; CAA67932.1, -.
InterPro; IPR00251, GT.11, -.
Pfam; PF01531; Glyco_transf_ll; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1502; DB 1; Length 340; Pred. No. 1.3e-119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 TFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK
                                                                                                                                                                                                                                                                                                         R -> H (IN REF. 3).
0629F1C04FC206AD CRC64;
                                                                                                                                                        CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       non-secretor phenotype.";
J. Biol. Chem. 270:4640-4649(1995).
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                                                                                                                                                                                                340
185
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1887 MW,
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79.6%;
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340 AA;
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Q10981;
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CYTOPLASMIC (POTENTIAL).

SIGNAL-ANGHOR (TYPE-TI MEMBRANE PROTEIN).

LUMENAL, CATALYTIC (POTENTIAL).

N-LINKED (GLCNAC. ...) (POTENTIAL).

N-LINKED (GLCNAC. ...) (POTENTIAL).

N-LINKED (GLCNAC. ...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Extensive polymorphism of the FUT2 gene in an African (Xhosa) population of South Africa."; hum. Genet. 103:204-210(1998).

-!- FUNCTION: CREADED THE PROCUSE PRECURSOR OLIGOSACCHARIDE FUC-ALPHA (1,2)GALBETA-) CALLED THE H ANTIGEN WHICH IS AN ESSENTIAL SOBSTRATE FOR THE FINAL STEP IN THE SOLUBLE A AND B ANTIGEN SYNTHESIS PATHMAY. HE AND SE BUXIMES FUCOSILATE THE SAME ACCEPTOR SUBSTRATES BUT EXHIBIT DIFFERENT KM VALUES.
-!- CATALYTICA CATILYTY: GDP-L-fucose + beta-D-galactosyl-R = GDP·+ alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
-!- PATHMAY: GlyCosylation.
-!- PATHMAY: GLYCOSYLAION. TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
[2]
SEQUENCE FROM N.A., AND VARIANT PHE-140.
MEDLINE=96199252; PubMed=8621666;
Kudo T., Iwasaki H., Nishihara S., Shinya N., Ando T., Narimatsu I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- ALTERNATIVE PRODUCTS: TWO FORMS ARE PRODUCED BY THE USE OF
ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.
-i- TISSUE SPECIFICITY: SMALL INTESTINE, CÓLON AND LUNG.
-i- MISCELLANBOUGS: THERE ARE TWO GENES (FUTI AND FUT2) WHICH ENCODE
GALACTOSIDE 2-L-POCOSYLTRANSFERASE THEY ARE EXPRESSED IN A
TISSUE-SPECIFIC MANNER WITH EXPRESSION RESTRICTED TO CELLS OF
MESODERNAL OR ENDODERNAL ORIGIN RESPECTIVELY.
-i- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY II.
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single missense
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Pfan: PP01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal-anchor; Golgi stack; Alternative initiation;
Blood group antigen; Polymorphism:
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND VARIANT PHE-140.
MEDLINE=97363210; PubMed=9219535;
Koda Y., Soejima M., Wang B., Kimura H.;
"Structure and expression of the gene encoding secretor-type
                                                                                                                                                           "Molecular genetic analysis of the human Lewis histo-blood
system. It. Secretor gene inactivation by a novel single mi
mutation A385T in Japanese nonsecretor individuals.";
J. Biol. Chem. 271:9830-9837(1996).
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/FTId=VAR_003422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T., du
                                                                                                                                                                                                                                                                                                                                                                                                                                                        galactoside 2-alpha-L-fucosyltransferase (FUT2).";
Eur. J. Biochem. 246:750-755(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu Y., Koda Y., Soejima M., Pang H., Schlaphoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SHORT ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LONG ISOFORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANTS VAL-25; CYS-138 AND ASN-172.
MEDLINE-98431007; PubMed-9760207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FORM IN TRANS CISTERNAE OF GOLGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, U17894; AAC24453.1; -.
EMBL; D89327; BAA13944.1; -.
EMBL; D87942; BAA21684.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                343
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beta-D-galactoside nal tract."; ses. .). : MEMBRÂNE PROTEIN) (GDP-L-fucose:beta-a(1,2)FT 2) FYRHLRPEILKEFT 180 ||||||||||||||||| ||YBHLRAEILQEFT 170 ALLTQCNHTIMTIG 300 VVADRGYLEKALDM 240 ndels 10; Gaps TOMSSGNTESPEMR 60 -----LEPATME 50 Tucose: beta-D-OCTENTIAL).
) (POIENTIAL).
) (POTENTIAL).
) (POTENTIAL).
) (POTENTIAL).
C64; Euteleostomi; Murinae; Mus. nsmembrane; ngth 344; awa M., ses.

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OR SECI OR RFT-II.
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                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 TAKKIPWQNYHINDMMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 RE--GMFTIRVKGRLGNQMGEYATLFALARMNGRLAFIPASMHSTLAPIFRISLPVLHSD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 PLAHFLIF--VFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGN 68
CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP + alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
PATHWAY: Glycosylation.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI (BY SIMILARITY).
MISCELLANBOUS: THERE ARE INO GENES (FUTL AND SEC1) WHICH ENCODE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 2 (EC 2.4.1.69) (Secretor blood group alpha-2-fucosyltransferase) (GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase 2) (Alpha(1,2)FT 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 GELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 AQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 VFVVISNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLIQCNHIIMTIGTFGIWAAY
                                                                                                                                                                                                                                                                                                                                  LUMENAL, CATALYTIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

4093E853E837303B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          67.1%; Score 1363.5; DB 1; Length 368; 75.9%; Pred. No. 7.5e-108;
                                                                                                                                                                                                                                                                       Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                      GALACTOSIDE 2-L-FUCOSYLTRANSFERASE.
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADL 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                354 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                    24; Mismatches
                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                          Pfam; PF01531; Glyco_transf_11; 1.
                                                                                                                                                                                                   EMBL; Y09882; CAA71008.1; -.
EMBL; AF11353; AAD25351.1; -.
MGD; MGI:109374; Fut2.
InterPro; IPR002516; GT_11;
                                                                                                                                                                                                                                                                                                                                                                                 41464 MW;
                                                                                                                                                                                                                                                                                    Signal-anchor; Golgī stack.
DOMAIN 1 20
                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Fucosyltransferase 2).
                                                                                                                                                                                                                                                                                                                                   42
195
195
289
315
368 AA;
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                                                                                                                                                                                                                                                                                                           21
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Q10983;
                                                                                                                                                                                                                                                                                                                                                                                                                                  258;
                                                                                                                                                                                                                                                                                                                                              CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
                                                                                                                                                                                                                                                                                                           FRANSMEM
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                                                                                                                                                                                                                                        Hitoshi S., Kusunoki S., Kanazawa I., Tsuji S.;

"Molecular cloning and expression of two types of rabbit beta-
galactoside alpha 1.2-fucosyltransferase.";

"Molecular cloning and expression of two types of rabbit beta-
galactoside alpha 1.2-fucosyltransferase.";

"Biol. Chem. 270:8644-8850(1995).

-I-FUNCTION: CREATES A SOLUBLE PRECURSOR OLIGOSACCHARIDE FUC-ALPHA
((1,2)GALBETA-) CALLED THE H ANTIGEN WHICH IS AND ESSENTIAL
SUBSTRATE FOR THE FINAL STEP IN THE SOLUBLE AND B ANTIGEN
SUBSTRATES BUT EXHIBIT DIFFERENT KM VALUES.

-I-CAPALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP-T-
alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!-PATHWAY: GLYCOSYLATION.
-!- PATHWAY: GLYCOSYLATION:
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
-!- FORM IN TRANS CISTERNAE OF GOLGI.
-!- TISSUE SPECIFICITY: SALIVARY AND LACTATING MAMMARY GLANDS.
-!- MISCELLANBOGS: THERE ARE THREE GENES (FUT1, FUT2 AND FUT3) WHICH
--- BNCODE GALACTOSIDE 2-L-FUCOSYLTRANSFERASE IN RABBIT. THEY ARE
--- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PWQNYHLNDWMSERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFL 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

1E2B831F9DA6CCB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.9%; Score 1319.5; DB 1; Length 354; 73.2%; Pred. No. 3.7e-104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR002516; GT_11.
Pfam; Pf01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47; Indels
                      Eukaryotā; Metazoa; Chòrdata; Craniata; Vertebrata; Eu:
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                 MEDLINE=95238380; PubMed=7721792;
   (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40035 MW;
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DOMAIN 1 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44
197
291
317
354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 248; Conserv
                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                        NCBI_TaxID=9986;
                                                                                                                                                                                   TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
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141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'n
                                                                                                                                                                                                                                                                                                                                                                                           Domino S.E., Hiraiwa N., Lowe J.B.;

Molecular cloning, chromosomal assignment and tissue-specific

expression of a murine alpha(1,2)fucosyltransferase expressed in
thymic and epididymal epithelial cells.";

thymic and epididymal epithelial cells.";

thymic and epididymal epithelial cells.";

Elochem J. 327:105:115(1997).

-!- CATALYHIG GEP-L-fucose + beta-D-galactosyl-R = GDP +
alpha-L-fucosyl-1,2-beta-D-galactosyl-R.

-!- PATHWAY: Glycosylation.

-!- PATHWAY: Glycosylation.

-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN: MEMBRANE-BOUND
FORM IN TRANS CISTERNAE OF GOLGI.

-!- SUBCELLULAR SOCIETIY: IN THE ADDIT, HIGHLY EXPRESSED IN PANCREAS,
C-!- TISSUE SPECIFICITY: IN THE ADDIT, HIGHLY EXPRESSED IN PANCREAS,
C-!- TISSUE SPECIFICITY: IN THE ADDIT, HIGHLY EXPRESSED

-!- SUBCELLANGE STREET AND EPIDIDMALS AND TO A LESSER EXTENT IN THYMUS, LONG

-!- MISCELLANGE STREET AND EPIDIOMARS AND UTERUS. NOT EXPRESSED

IN BRAIN, HERRY, SKELETAL MUSCLE, KIDNEY, LIVER AND BONE MARROW.

-!- MISCELLANGOUS THERE ARE TWO GENES (FUII AND FUT2) WHICH ENCODE

-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                              15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 1 (EC 2.4.1.69) (GDP-L-fucose:beta-
D-galactoside 2-alpha-L-fucosyltransferase 1) (Alpha(1,2)FT 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
LUMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
252 SNGMAWCRENIDASRGDVVFAGNGLEGSPAKDFALLFQCNHTVMTIGTFGFWAAYLTGGD 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 LTLSVLCSDYHLLK-SPVAMVCLPHPLQTSNGSPSCPEQ-----SSSLSGTWTITPG 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 VISTIIHLQORIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSI
                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:109375; Fut1.
InterPro; IPR002516; GT_11.
Pfam: PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL)
                              314 TIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLL 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1107; DB 1;
Pred, No. 3.6e-86;
                                               376 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97454449; PubMed=9355741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             328 N. 42255 MW;
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60.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U90553; AAC53492.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Golgi stack.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 210; Conservative
                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                           (Fucosyltransferase 1).
                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27
67
302
328
328
376 AA;
                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
STRAIN=NIH Swiss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal-anchor;
DOMAIN
                                                                                                                                    FUT1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
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                                                                                                                      FUT1_MOUSE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1996 (Rel. 34, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 1 (EC 2.4.1.69) (GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase 1) (Alpha(1,2)FT 1)
GRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 CRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLAN 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. J. 30.:23-626(1994).

-!- CATALYTY CACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP + alpha-L-fucosyl-1,2-beta-D-galactosyl-R.

-!- PATHWAY: Glycosylation.
-!- PATHWAY: Glycosylation.
-!- PATHWAY: Glycosylation.
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BCUND FORM IN TRANS CISTERNAE OF GOLGI (BY SIMILARITY).
-!- MISCELLANBOUG: THERE ARE TWO GENES (FUT1 AND FUT2) WHICH ENCODE GALACTOSIDE 2-L-FUCOSYLTRANSFERASE. THEY ARE EXPRESSED IN A TISSUE-SPECIFIC MANNER MITH EXPRESSION RESTRICTED TO CELLS OF
                                                           NDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLAVNG
                                                                                                                                                                                                                                          149 HDWMSEEYSHLEDPFLKLSGFPCSWTFFHHLREQIRREFTLHNHLREGAQYLLSGLRIGP
                                                                                                                                                                                                                                                                                                                           SQPS-IFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAW
                                                                                                                                                                                                                                                                                                                                                                                                    209 ASPAHTFVGVHVRRGDYLEVMPNRWKGVVGDRAYLQQAMDWFRARHKDPIFVVTSNGMKW
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-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plau J.-P., Labarriere N., Dabouis G., Denis M.G.;
Evidence for two distinct alpha(1.2)-fucosyltransferase
differentially expressed throughout the rat colon.";
Biochem. J. 300:623-626(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Two distinct rat GDP-L-fucose:b-D-galactoside 2-alpha-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       329 FTLPDSEFLKIFRPEAAFLPEWVGINADLSPLQAQFDPWKPDSLFRL 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       320 YTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLKALTPACPRSHFHL 366
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Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 376 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soejima M., Wang B., Koda Y., Kimura H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94280382; PubMed=8010942;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Fucosyltransferase 1). FUT1 OR FTA.
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FUTI_HUMAN
ID FUTI_H
DT 01-FEB
DT 01-FEB
DT 01-FEB
DT 05-FUN
DE Galact
DE D-galact
GN FUTI.
                                                                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 1 (EC 2.4.1.69) (GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase 1)
                                                                                                                                                                                                                                                     GRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHL 140
                                                                                                                                                                                                                                                                                                   141 NDWMBERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVN- 199
                                                                                                                                                                                                                                                                                                                         207
                                                                                                                                                                                                                                                                                                                                                258
                                                     CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-11 MEMBRANE PROTEIN)
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                         21 VISTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSI 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- TISSUE SPECIFICITY: BRAIN.
-!- MISCELLANEOUS: THERE ARE TWO GENES (FUT1 AND FUT2) WHICH ENCODE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- PATHWAY: Glycosylation.
-i- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
                                                                                                                                                                                                                       148 HDWMSEEYSHLEDPFLKLSGFPCSWTFFHHLREQIRREFTLHDHLREDAQRLLSGLRIGP
                                                                                                                                                                                                                                                                                                                                                -GSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMA
                                                                                                                                                                                                                                                                                                                                                                                             WCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                     (LOMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     = GDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MINISTRY C. KUSHOKUS, KENAZAWA I., TSHJI S.,
"MOLECULAR CLORING and expression of two types of rabbit beta-
galactoside alpha 1,2-fucosyltransferase.";
J. Biol. Chem. 270:8844-8850(1995).
-:- CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = G
        Interpro; IPR002516, Gr. 11.
Pfam, PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                           54.2%; Score 1102; DB 1; Length 376; 60.1%; Pred. No. 9.6e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLKALTPACPRSHFHL 366
                                                                                                                                                                                  Indels
                                                                                                                                    C350C737C758B7F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       373 AA
                                                                                                                                                                      Pred. No. 9.66
                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FORM IN TRANS CISTERNAE OF GOLGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Brain;
MEDLINE=95238380; PubMed=7721792;
                                                                                                                                     MW.
                                            stack
                                                                                                                                     42416
 EMBL; L26009; AAB41514.1;
                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Fucosyltransferase 1).
                                                                                                  64
302
                                            Golgi
                                                                                       30 3
64 · 3
302 3
328 3
376 AA;
                                                                                                                                                                      Local Similarity
es 209; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9986;
                                            Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUT1 OR RFT-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUT1_RABIT
Q10979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia;
                                                                                                     CARBOHYD
                                                                                                              CARBOHYD
                                                                                                                            CARBOHYD
                                                                                                                                    SEQUENCE
                                                                   TRANSMEM
                                                                                                                                                            Query Match
                                                      DOMAIN
                                                                                          DOMAIN
                                                                                                                                                                        Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
FUT1_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                  268
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01-FBB-1991 (Rel. 17, Last sequence update)
15-JON-2002 (Rel. 41, Last annotation update)
6alactoside 2-L-fucosyltransferase 1 (EC 2.4.1.69) (GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase 1)
(Rucosyltransferase 1) (Alpha(1,2)FT 1)
(Kucosyltransferase 1) (Blood group H alpha 2-fucosyltransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMBERYRHIPGHFVRFTGYPCSWTFYHH 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------DMITOMS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRPEILKEFTLHOHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVV
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                    OF.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LUMENAL, CATALYTIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL)

N-LINKED (GLCNAC. .) (POTENTIAL)

N-LINKED (GLCNAC. .) (POTENTIAL)

OA47A1786231525C CRC64;
                    TISSUE-SPECIFIC MANNER WITH EXPRESSION RESTRICTED TO CELLS MESODERMAL OR ENDODERMAL ORIGIN RESPECTIVELY.
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41;
                                                                                                                                                                                                                                                                                                                                           Interpro; IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1086.5; DB 1; Length 373; Pred. No. 1.9e-84;
GALACTOSIDE 2-L-FUCOSYLTRANSFERASE. THEY ARE EXPRESSED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                         Signal-anchor; Golgi stack.
DOMAIN 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 57.65
Matches 209; Conservative
                                                                                                                                                                                                                                                                                                                      EMBL; X80226; CAA56513.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      252
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66
301
327
373 AA;
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P19526;
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CARBOHYD
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- PATHWAY: Glycosylation.
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.
-!- POLYMOREHISM: NONFUNCTIONAL MUTANT OF FUT1 ARE THE CAUSE OF THE H-BOMBAY BLOOD GROUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
LUMENAL, CATALYIC (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
Y -> C (IN BOMBAY H-).
                                                                                                                                                                                                                                                                                                                                                 Larsen R.D., Ernst L.K., Nair R.P., Lowe J.B.;
"Modecular Cloning, sequence, and expression of a human GDP-L-flucose:beta-D-galactoside 2-alpha-L-flucosyltransferase cDNA that can form the H blood group antigen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- MISCELLANEOUS: THERE ARE TWO GENES (FUT1 AND FUT2) WHICH ENCODE GALACTOSIDE 2-L-FUCOSYLTRANSFERASE. THEY ARE EXPRESSED IN A TISSUE-SPECIFIC MANNER WITH EXPRESSION RESTRICTED TO CELLS OF MESOBERMAL OR ENDODERMAL, ORLGIN RESPECTIVELY.
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                                                           \text{LOWe J.B.;} "Molecular basis for H blood group deficiency in Bombay (Oh) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM; 211.00; -.
InterPro; IPR002516; GT_11.
Pfam: PF0131; Glyco_transf=11; 1.
Fransferase; Glycosyltransferase; Glycoprotein; Iransmembrane;
Signal-anchor; Golgi stack; Polymorphism; Blood group antigen.
DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).
TRANSMEM 9 25 SIGNAL-ANCHOR (TYPE-II MEMBRANE PI DOMAIN 26 365 LUMENAL, CATALYTIC (POTENTIAL).
CARBOHYD 527 327 N-LINKED (GLCNAC. ..) (POTENTIAL VARIANT 154 154 Y -> C (IN BOMBAY H-).
                                                                                                                                                                                                                                       MEDLINE=94286534; PubMed=7912436;
Kelly R.J., Ernst L.K., Larsen R.D., Bryant J.G., Robinson J.S.
Lowe J.B.;
                                                                                                                                                                                     ō
                                                                                                                                                                                "Polymorphism of the h allele and the population frequency sporadic nonfunctional alleles."; Transfusion 37:284-290(1997).
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 87:6674-6678(1990)
                                                                                                                                                                                                                                                                                                   para-Bombay individuals.";
Proc. Natl. Acad. Sci. U.S.A. 91:5843-5847(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                             [2]
SEQUENCE FROM N.A., AND VARIANT ALLELES.
MEDLINE=97240210; PubMed=9122901;
                                                  MEDLINE=90370848; PubMed=2118655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M35531; AAA52639.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z69587; CAA93435.1; -. PIR; A36047; A36047. Genew: HGNC:4012; FUT1.
                                                                                                                                                                      Wagner F.F., Flegel W.A.;
                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     VARIANT HIS-164.
            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                          VARIANT ARG-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM; 211100;
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029043; 019101;
01-NOV-1997 (Rel. 35, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 1 (EC 2.4.1.69) (GDP-L-fucose:beta-
D-galactoside 2-21pha.L-fucosyltransferase 1) (Alpha(1,2)FT 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 IFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEIL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 REFTLHDHLREEAQSVLGQLRLGRTGDRPRTFVGVHVRRGDYLQVMPQRWKGVVGDSAYL 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 PEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-----QH-PASLSGTWTVYPNGRFGNQMGQYATLLALAQLNGRRAFILPAMHAALAP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295 TIMTIGTFGIWAAXLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLKA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 LAFLLVCVLSVIFFLHIHQDSFPHGLGLSILCPDRRLVTPPVAIFCLPGTAMGPNASSSC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                              ------RIVKLQPLSEKELPMTIQMSSGNTES 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 KEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYL
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96217559; PubMed=8613146;
Cohney S., Mouhtouris E., McKenzie I.F., Sandrin M.S.;
"Molecular cloning of the gene coding for pig alghal-->2
                                                                                                                                                                                                                                                                                                                                                                                                87; Indels
                                                                                                            L -> R (IN BOWBAY H-).
/FIId=VAR_009709.
/ V -> E (IN BOWBAY H-).
/FIId=VAR_019419.
A -> V (IN BOWBAY H-).
/FIId=VAR_019420.
/FIId=VAR_019421.
/FIId=VAR_019421.
W -> C (IN BOWBAY H-).
/FIId=VAR_019421.
/FTId=VAR_003417.
L -> H (IN PARA-BOMBAY).
/FTId=VAR_009708.
W -> C (IN BOMBAY H-).
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                                                                                                                                                                                                                                                                                                                                                  52.0%; Score 1057.5; DB 56.5%; Pred. No. 5.4e-82
                                                                        W -> C (IN BOMBAY
/FTId=VAR_003418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               365 AA
                                                                                                                                                                                                                                                                                                                                                                                                46; Mismatches
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                                                                                                                                                                                                                                                                                                       41251 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                         12 LAHFLIFVFVTSTIIHLQQ---
                                                                                                                                                                                                                                                                                                                                                                                                Matches 205; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                          164
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                                                                                                                                                                                                                                                                                                     365 AA;
                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9823;
                                                                                                                                                                                                                                                         349
                          164
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                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                             Best Local
                          VARIANT
                                                                     VARIANT
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290 PARDFALLVQCNHTIMTIGTFGFWAAYLAGGDTIYLANFTLPTSSFLKIFKPEAAFLPEW 349

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                                                                                                                                                                                                                               40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN),
LUMENAL, CATALYTIC (POTENTIAL).
LUNED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 PMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 PVAIFCLAGTPVHPNASDSCPKH-PASLSGTWTIYPDGRFGNQMGQYATLLALAQLNGRQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 AFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWIFYHHLRPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMP 221
                                                                                                                                           Meijerink E., Neuenschwander S., Fries R., Dinter A.,
Meijerink E., Neuenschwander S., Fries R., Dinter A.,
Bertschinger H.O., Stranzinger G., Vogegali P.;
Bertschinger H.O., Stranzinger G., Vogegali P.;
Expression and activity of porcine alpha1,2) fucosyltransferases
determine erythrocyte antigen precursor O status and susceptibility t
Escherichia coli FIB colonization in the small intestine.",
Submitted (MAR.1999) to the EMBL/GenBank/DDBJ databases.
1. CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP +
alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Meijerink E., Fries R., Voegeli P., Masabanda J., Wigger G., Stricker C., Newenschwander S., Bertschinger H.U., Stranzinger G.; Two alpha(1,2) fucosyltransferase genes on porcine chromosome 6q11 are closely linked to the blood group inhibitor (S) and Bscherichia coli F18 receptor (ECRIBR) loci."; Mamm. Genome 8:736-741(1997).
                                                                                                                                                                                                                                                                                                               -!- PATHWAY: Glycosylation.
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.
-!- MISCELLANEOUS: THERE ARE IWO GENES (FUTI AND FUT2) WHICH ENCODE GALACTOSIDE 2-L-FUCOSYLTRANSFERASE. THEY ARE EXPRESSED IN A TISSUE-SPECIFIC MANNER.
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWIFFHHLREQIRSEFTLHDHLRQEAQGVLSQFRLPRIGDRPSIFVGVHVRRGDYLRVMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.7%; Score 1050.5; DB 1; Length 365; 62.9%; Pred. No. 2.1e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -> F (IN REF. 1).
DAFCE77E89A29D75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Golgi stack; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41106 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L50534; AAB02984.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB81884.1; -.
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InterPro; IPR002516; GT_11.
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365
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65
301
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365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                t Local Similarity
ches 195; Conserv
                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U70883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
CARBOHYD
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL cutstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUC-ALPHA (1.2) GALBETA-) CALLED THE HANTGEN WHICH IS AN BSSENTIAL SUBSTRATE FOR THE FINAL STEP IN THE MEMBRANE-ASSOCIATED A AND B ANDIGEN SYMPHESIS PATHWAY. HAND SE BUZYMES FUCOSYLATE THE SAME ACCEPTOR SUBSTRATES BUT EXHIBIT DIFFERENT KN VALUES.

-!- CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP + alpha-L-fucosyl-1.2-beta-D-galactosyl-R.
-!- PATHWAY: Glycosylation.
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: TYPE IYONG SIMILARITY).
-!- SUBCELLULAR SET SIMILARITY IN SIMILARITY IN SIMILARITY.
-!- SUBCELLULAR SIMILARITY IN SIMILARITY IN SIMILARITY.
-!- SUBCELLULAR SIMILARITY IN SIMILARITY IN SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                282 PAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEW 341
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ದಿದ್ದರ್ಭ
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                                                                                                                                                                                                                                                           (Secretor blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . .) (POTENTIAL)
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O
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"Evidence for two distinct alpha(1,2)-fucosyltransferase genes
differentially expressed throughout the rat colon.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
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                                                                                                                                                                                   01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
115-JUN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase) (GD2 (EC 2.4.1.69) (Secreting Troup alpha-2-fucosyltransferase) (GD2-L-fucose:Deta-D-galactoside 2-alpha-L-fucosyltransferase 2) (Alpha(1,2)FT:
(Fucosyltransferase 2) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the Swiss Institute of Bioinformatics and the pean Bioinformatics Institute. There are no remon-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. J. 300:623-626(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14DECEB7C2E6384A CRC64;
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                                                                                                                                                 159 AA
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                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94280382; PubMed=8010942;
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                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
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342 VGIPADLSPL 351
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                                   350 VGINADLSPL
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the European
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                                                                                                                                                 FUT2_RAT
Q10984;
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                                                                                                         RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wilson R., Ainscough R., Adderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Sims M., Smaldon N., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
61 PAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEW 120
                                                                                                                                                                                                                         01-FEB-1994 (Rel. 28, Created)
15-JON-2002 (Rel. 41, Last sequence update)
15-JON-2002 (Rel. 41, Last annotation update)
Putative glycosyl transferase C06E1.7 in chromosome III (EC 2.-.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 SIGRLGNQMGEYATLFALARMNGR--LAFIPASMHNALAPIFRISLPVLHSD----- 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 STARLANHIFELVSVYGMAKSLNRKPAIFVEDSKYNLLITGVRKVLPGLLDEFQIFEYPV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 --TAKKIP------WQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 TLHDHVREEAQAFLRGL----RVNGSQPSTFVG---VHVRRGDYV---HVMPNVWKGVVA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             '2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waterston R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 365; 7.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48; Mismatches 115; Indels
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InterPro, IPR005516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Hypothetical protein; Transferase; Glycosyltransferase.
SEQUENCE 365 AA: 41991 MW; B5FBCA363F31977F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           342 VGIPADLSPLLKALTPACPRSHFHLKAKGVTCYVAGRAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Bristol N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L16559; AAA27932.2; -.
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                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wohldman P.;
                                                                                                                                                                                  YKQ7_CAEEL
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91082407; PubMed=1845921; Plowes C.C., Eastman E.M., O'Callaghan D.J.; Plowers C.C., Eastman E.M., O'Callaghan D.J.; "Sequence analysis of a glycoprotein D gene homolog within the unique short segment of the EHV-1 genome.";
---DKYKEKVQSFVKPAIDFSPLPNSDSSNFISRICIHIRRTDFVDGQHHSSNV---- 223
                                                                --YSSPVFVVTSNGMAWCRENINASRGD 270
                                                                                                                                                                                271 VVFAGNGIEGSPAKDFALL-TQCNHTIMTI--GTFGIWAAYLAGGDTIYLANY-TLPDSF 326
                                                                                                                                                                                                                      MEDINE-92263758; PubMed=1316673; Colle C.F. III, Flowers C.C., O'Callaghan D.J.; Colle C.F. III, Flowers C.C., O'Callaghan D.J.; Colle C.F. III, Flowers encoding a protein kinase, homolog of glycoprotein gx of pseudorables virus, and a novel glycoprotein map within the unique short segment of equine herpesvirus type 1."; Virology 188:545-557(1992).
                                                                                                                   --SFIKPALEFIKEREQKDVNKKMLTVIMGDDPDFEAKMF----EGTVRAKKEAKIEETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. ) (POIENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
323CDCA9C9762F05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENȚIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Equine herpesvirus type 1 (strain Kentucky A) (EHV-1).
Viruses; dSDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glycoprotein D precursor (Glycoprotein 17/18)
GD OR GP17/18 OR 72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLYCOPROTEIN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             442 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 91; DB
Pred. No. 3.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
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PIR, A38518, VGBEEA.
InterPro, IPRO02896; Herpes_glycop_D.
Pfam; PF01537; Herpes_glycop_D; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
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EMBL; M87497; AAA46073.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                          327 FLK-VFKPEAAFLPEWVGIPAD 347
                                                                                                                                                                                                                                                                                                                                                                   335 YKKGVLDPDDFFVPSWTSIMLD 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49908 MW;
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SIGNAL 1
                                                         230 DRGYLEKALDMFRAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              347
396
442 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VGLD_HSVEK
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TRANSMEM
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VGLD_HSVEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAJOR FIMBRIAL SUBUNIT PROTEIN, TYPE III.
                                                                                                                                                                                         136 QNYHLNDWMEERYRH----IPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQ 190
                                                                                                               78 NSIGRLGNQMGEYAT--LFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPW 135
                                                                                                                                                         ----FARPVPP 331
                                                                                                                                                                                                                                 DNHPGFDSVESEITQNKTDPKFGQADPKPNQPFKWPSIKHLVPRL-----DEVDEVIE 384
                                                                         LYRRVIEIDGRRIYTDFSVTIPSERCPIAFELNFGN---PDRCKTPEOYSRGE---VFTR 287
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fujiwara T., Morishima S., Takahashi I., Hamada S.,
"Molecular cloning and sequencing of the fimbrilin gene of
Porphyromonas gingivalis strains and characterization of recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION. Finbrillin is the structural subunit of the fimbriae, that are filamentous appendages on the cell surface. Funbriae of P. gingivalis are recognized as a major virulence factor as they mediate cell adhesion and play an important role in invasion of
                                     LQQRIVKLQ------PLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTI 77
                                                                                                                                                                                                                                                                   191 AFLRGLRVNGSOPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSP 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional differences among FimA variants of Porphyromonas gingivalis and their effects on adhesion to and invasion of human epithelial cells.";
Infect. Immun. 70:277-285(2002).
                                                                                                                                                                                                                                                                                             385 PVIKPPKTSKSN-STFVGISVGLGIAGLVLVGVILYVCLRR---KKELKVCTERLDSP
                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Major fimbrial subunit protein, type III precursor (Fimbrillin)
   50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE P.GINGIVALIS FIMBRILLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nakagawa I., Amano A., Kuboniwa M., Nakamura T., Kawabata S.
Hamada S.;
 31; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7FBE4FBF427EA2AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides; Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochem. Biophys. Res. Commun. 197:241-247(1993).
                                                                                                                                                     288 RFLGEFNFPQGEHMTWVKFWFVYDGGNL---PVQFYEAQA--
                                                                                                                                                                                                                                                                                                                                                                                                       353 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION, AND CLASSIFICATION INTO TYPES.
                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21614934; PubMed=11748193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          periodontal tissues.
SUBCELLULAR LOCATION: Fimbria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Porphyromonadaceae; Porphyromonas.
NCBI_TaxID=837;
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 Conservative
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353 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Fimbrilin).
                                                                                                                                                                                                                                                                                                                                                                                                     FMA3_PORGI
051826;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteins
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MEDLINE=20139694; PubMed=10673428;
Hallberg B.M., Bergfors T., Boeckbro K., Pettersson G., Henriksson G.,
                                                                                                                                                                                              80 LTTELTEGNQEAAGLIMTAEPVEVTLVAGN-----NYYGYDGSQGGNQISQGTPLE 130
                                                                                                                                                                                                                                                                                                                                   --KEFTLHDHV----REEAQAFLRGLRVNGSQPSTF--VGVHVRRGDYVHVMPNVWKGVV 228
                                                                                                                                                                                                                                                                                                                                                                         246 VKGKLTKHDGTALSSEEMTAAFNAGWIVANNDPTTYYPVLVNFESNNYTYTGEAVEKGKI 305
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                                                 Gaps
                                                                                     45 MITQMSSGNTESPEMRRDSEQ-----HGNGELRGMFTINSIGRLGNQMG---EYAILFA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Basidiomycota; Hymenomycetes; Homobasidiomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDH_PHACH STANDARD; PRT; 773 AA.
001738; 000047;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
cellobiose dehydrogenase precursor (EC 1.1.5.1) (CDH) (Cellobiose-
                                                                                                                                                                                                                                                    ----IPWQNYHLNDWMEERYRHI-----PGHFVRFTGYPCSWTFYHH--LRPEIL-
                                                                                                                                                                                                                                                                                          191 TTFNGAYSPANYTHVDWLGRDYTEIGAATVNTFKGF----YVLESTYAQNAGLRPTILC
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                                               78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97176414; Pubmed-9023960;
Li B., Nagalla S.R., Renganathan V.;
"Cellobiose dehydrogenase from Phanerochaete chrysosporium is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A new scaffold for binding haem in the cytochrome domain of extracellular flavocytochrome cellobiose dehydrogenase."; Structure 8:79-88(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                229 ADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGI 278
                                                                                                                                                                                                                                                                                                                                                                                                                                            306 VRNHKFDINLTITGPGTNNPENPIT-----ESANLNVNCVVAAWKGV 347
Score 89; DB 1; Length 353;
Pred. No. 3.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li B., Nagalla S.R., Renganathan V.; "Cloning of a cDNA encoding cellobiose dehydrogenase, hemoflavoenzyme from Phanezochaete chrysosporium."; Appl. Environ. Microbiol. 62:1329-1335(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Secreted.
SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO
                                          Mismatches 110;
                                                                                                                                                                    LARMNGRLAF - - I PASMHNALAPIFRISLPVLHSDTAKK - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Basidiomycota; Hymenomycete
Aphyllophorales; Corticiaceae; Phanerochaete.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Appl. Environ. Microbiol. 63:796-799(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: Cellobiose + a lactone + a phenol.
-!- COFACTOR: ONE FAD AND ONE HEME B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97077226; PubMed=8919793;
                                            38;
                       22.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phanerochaete chrysosporium.
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                                               Conservative
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    Query Match
Best Local Similarity
Matches 64; Conserv
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between the Swiss Institute of Bioinformatics and the EMBL outstation-
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                Ouery Match 4.4%; Score 89; DB 1; Length 773; Best Local Similarity 22.0%; Pred. No. 9.3; Matches 49; Conservative 29; Mismatches 91; Indels
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Gaps

54;

153 GHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREBAQAFLRG------LRVNGSQPS 204

Search completed: May 27, 2003, 15:07:12 Job time : 22.122 secs

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VICTOR TO I	- 2003	
פעוניסדע	(c) 1993 - 2003 Compu	
	Copyright	

OM protein - protein search, using sw model

May 27, 2003, 14:52:27 ; Search time 45.4049 Seconds	<pre>(without alignments) 1050.630 Million cell updates/sec</pre>	000 CC WGOOD - C800 OF - O10 - O1 - O11
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US-10-040-863-8_COPY_23_380 s: 1921 l STITHLOQRIVKLQPLSEKERSHFHLKAKGVTCYVAGRAF 358	BLOSUM62
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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			Description		Rat henatoma Has o	Rat heratoma H35 c	Rat honatoma 1135 c	Dat honatoms 1135 c	nar neparoma ass c	Did sound of Cut	Himan Cood protoin	Human secz protern	GDD-Fug.bots-D-23	GDP-L-fucose-beta-
CHINGINGO			ID	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	AAB36104	AAE16622	AAB36105	AAE16623	AAW37855	AAW53103	AAW69332	AAB36106	AAR13751	AAR80154
			DB	1	21	23	21	23	5	16	6	21	12	16
			Match Length DB		380	380	353	353	340	340	343	344	365	365
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		Result	NO.	1 1 1 1 1	Н	2	m	4	'n	9	7	80	9	10

New rat ganglioside GM1-specific alpha1-2Fucosyltransferase, useful for

(PACI-) PACIFIC NORTHWEST CANCER FOUND.

Holmes EH, Sherwood AL; WPI; 2000-687262/67. N-PSDB; AAC67965.

	-fucosylt	-Alpha-fucosvitr	uman H-transfera	uman albha 1,2 f	n alpha(1,2)-	an H-transfer	id H transferase	ig albha-1-2 f	ne alpha (1.2)	wine alpha(1.2	alpha-1.2-f	qlvcosvltransfe	jaevis alpha-1	an secreted	ri UA802 a	cobacter pylo	ceroides fragi	ropionibacterium	uman protein c	th Factor Rec	, elegans alpha	ovel human dlagn	human diag	n polypeptide	cid sequer	acteriu	Comonas	protein seg	l signal tı	odenesis asso	human prot	L human s	e ischaemic	l human di	2. Hō
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ALIGNMENTS

RESULT 1

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Rat; alphal-2fucosyltransferase; cytostatic; neuroprotective; nootropic; gene therapy; Fucalphal-2Galbetal-3GalNAc; immunotherapy; immunosuppression; cancer; neurological disease; small cell lung carcinoma.
                                                         Rat hepatoma H35 cell alphal-2fucosyltransferase.
     AAB36104 standard; Protein; 380 AA.
                                                                                                                                                                          99WO-US07384.
                                                                                                                                                                                            99WO-US07384.
                                         (first entry)
                                                                                                                      Rattus norvegicus.
                                                                                                                                       WO200064464-A1.
                                                                                                                                                                          23-APR-1999;
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                                         19-FEB-2001
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                       AAB36104;
AAB36104
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                                                           The present sequence was given in a specification relating to an isolated rat ganglioside GM_1-specific alphal-2fucosyltransferase protein. The protein or its cellular fraction is useful for synthesis of a molecule comprising Fucalphal-2Galbetal-3GalNAc, a glycolipid, glycoprotein, glycolipoprotein or a free oligosaccharide comprising alphal-2fucosyltransferase with GDP-fucose and a molecule or glycolipid, alphal-2fucosyltransferase with GDP-fucose and a molecule or glycolipid, glycolipoprotein or oligosaccharide having a terminal glycoprotein, glycolipoprotein or oligosaccharide having a terminal composition the protein with GDP-fucose and ganglioside GM_1. The contacting the protein with GDP-fucose and ganglioside GM_1. The contacting the protein with GDP-fucose and ganglioside GM_1. The contacting the protein with GDP-fucose and ganglioside GM_1. The contacting the protein with GDP-fucose and ganglioside GM_1. The contacting the protein and introducting an immunotherapeutic or immunosuppressive action against cancer, neurological disease or small cell lung carcinoma.
                                                                                                                                                                                                                                                                                                                 0
   useful as a nutritional composition neurological diseases -
                                                                                                                                                                                                                                                                                                                                                                                61 LGNQMGEYATLFALARMNGRLAFIPASMENALAPIFRISLPVLHSDTAKKIPWQNYHUND 120
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                                                                                                                                                                                                                                                                                                                                                                                                WMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTL 300
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                                                                                                                                                                                                                                                                                                                                                 Rat; alphal-2fucosyltransferase; alphal-2fucT; antisense therapy; galactose betal-3N-acetylgalactosamine; Galbetal-3GalNAc; glycolipid; glycoprotein; glycolipoprotein; oligosaccharide; fucosyl-GM1; cancer; gene therapy; oncogenic transformation; cytostatic; ganglioside; GM1;
                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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/note= "Intracellular/Transmembrane domain"
199
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                                                                                                                                                                                                                                                                                   Score 1921; DB 21;
Pred. No. 2.7e-201;
Mismatches 0;
preparation of fucosyl GM1 which is
or immunotherapeutic for cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H35 cell alphal-2FucT.
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100.0%;
                                      Claim 1; Fig 5; 91pp; English
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358; Conservative
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                                                                                                                                                                                                                                                         Sequence
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Best Local 9
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Matches
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The invention relates to rat GML-specific alphal-2fucosyltransferase (alphal-2FucT) enzyme and its corresponding nucleic acid. This nucleic acid is specific for a carbohydrate moiety found in ganglioside GML, a terminal galactose betal-3N-acety/galactosamine (albetal-3GalNac) saccharide. Alphal-2FucT DNA is useful for producing rat alphal-2FucT protein by recombinant techniques. Alphal-2FucT DNA is useful for the preparative synthesis of fucosyl containing glycolipids, glycolipids, glycolipids, glycolipids, glycolipids, glycolipids, glycolipids assaying for changes in expression of alphal-2FucT DNA is useful for detecting oncogenic transformation which involves assaying for changes in expression of alphal-2FucT is activated in cell transformation, antisense sequences derived from alphal-2FucT DNA are useful for inhibiting, suppressing or treating cancer. Alphal-2FucT DNA is useful in gene therapy and alphal-2FucT DNA is useful in gene therapy and alphal-2FucT DNA is useful in gene therapy and alphal-2FucT DNA are useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat hepatoma H35 celi alphal-2fucosyltransferase, useful for producing GMJ-specific alphal-2fucosyltransferase enzyme by recombinant techniques and for detecting oncogenic transformation of test tissues .
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/note= "N-glycosylated"
221..380
/note= "Region which overlaps rat FTB"
                                                                                                              /note= "N-glycosylated"
                                                                                                                                                                      /note= "N-glycosylated"
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N-PSDB; AAD27207.
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323 PDSPFLKVFKPEAAFLPEWVGIPADLSPLLKALTPACPRSHFHLKAKGVTCYVAGRAF 380

Wed May 28 09:22:53 2003

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Claim 4; Fig 3; 41pp; English
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                                                                                                                                                                                                                                                                                                         (first entry)
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238
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N-PSDB; AAD27208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is given in a specification relating to a rat ganglioside GM 1-specific alphal-2fucosyltransferase protein. The protein or its cellular fraction is useful for synthesis of a molecule comprising recalphal-2Galbetal-3GalNac, a glycolipid, glycoprotein, glycolipoprotein or a free oligosaccharide comprising Fucalphal-2Galbetal-3GalNac. The method involves contacting alphal-2fucosyltransferase with GDP-fucose and a molecule or glycolipid, glycoprotein, glycolipoprotein or oligosaccharide having a terminal Galbetal-3GalNac group. It is also useful for synthesis of fucosyl-GM_1 by contacting the protein with GDP-fucose and ganglioside GML1. The obtained glycoproteins, glycolipids and oligosaccharides are useful as nutritional compositions and fucosyl-GM_1 is useful for inducing an intrinsical compositions and fucosyl-GM_1 is useful for inducing an intrinsical compositions and fucosyl-GM_1 is useful for inducing an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New rat ganglioside GMI-specific alphal-2Fucosyltransferase, useful for preparation of fucosyl GMI which is useful as a nutritional composition or immunotherapeutic for cancer and neurological diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWWEBR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 YRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFV 185
                                                                                                                                                                        Rat; alphal-2fucosyltransferase; cytostatic; neuroprotective; nootropic; gene therapy; Fucalphal-2Calbetal-3GalNAc; immunotherapy; immunosuppression; cancer; neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LOORIVELOFILSEKELPMITQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM 60
                                                                                                                                     Rat hepatoma H35 cell alphal-2fucosyltransferase catalytic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 LQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunotherapeutic or immunosuppressive action against cancer, neurological disease or small cell lung carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.7%; Score 1896; DB 21; 100.0%; Pred. No. 1.3e-198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
O
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                                                                                                                                                                                                                                                                                                                                                                                                                                        (PACI-) PACIFIC NORTHWEST CANCER FOUND.
                                AAB36105 standard; Protein; 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Fig 3A; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US07384
                                                                                                                                                                                                                                                                                                                                                                      99WO-US07384
                                                                                                      (first entry)
                                                                                                                                                                                                                                lung carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sherwood AL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-687262/67.
N-PSDB; AAC67966.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 353; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     353 AA;
                                                                                                                                                                                                                                                               Rattus norvegicus
                                                                                                                                                                                                                                                                                                WO200064464-A1.
                                                                                                                                                                                                                                                                                                                                                                      23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                     23-APR-1999;
                                                                                                    19~FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Holmes EH,
                                                                   AAB36105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
RESULT 3
              AAB36105
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(alphal-2Fucr) enzyme and its corresponding nucleic acid. This nucleic acid is specific for a carbohydrate moiety found in ganglioside GM1, a terminal galactose betal-3N-acetylgalactosamine (Galbetal-3GalNAC) saccharide. Alphal-2Fucr DNA is useful for producing rat alphal-2Fucr protein by recombinant techniques. Alphal-2Fucr DNA is useful for the preparative synthesis of fucosyl containing glycolipids, glycoproteins, glycolipoproteins and oligosaccharide, and for preparing fucosyl-GM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat hepatoma H35 cell alphal-2fucosyltransferase, useful for producing GMl-specific alphal-2fucosyltransferase enzyme by recombinant techniques and for detecting oncogenic transformation of test tissues
186 GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS 245
                                                                                                                                                        305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat; alphal-2fucosyltransferase; alphal-2FucT; antisense therapy; galactose betal-3Nacetylgalactosamine; Galbetal 3GalNac; glycolipid; glycoprotein; glycoprotein; olipoprotein; oliposaccharide; fucosyl-GMI; cancer; gene therapy; oncogenic transformation; cytostatic; ganglioside; GMI; cell transformation; catalytic Gomain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to rat GMI-specific alphal-2fucosyltransferase
                                          RGDVVFAGNGIEGSPAKDFALLIQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF
                                                                                                                                                                                                                                                                                                                                            306 LKVFKPEAAFLPEWVGIPADLSPLLKALTPACPRSHFHLKAKGVTCYVAGRAF 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Region which overlaps rat FTB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H35 cell alphal-2FucT catalytic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE16623 standard; Protein; 353 AA
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6
Alphal-2FucT DNA is useful for detecting oncogenic transformation which
           involves assaying for changes in expression of alphal-2 FucT. Since alphal-2FucT is activated in cell transformation, antisense sequences derived from alphal-2FucT DNA are useful for inhibiting, suppressing or treating cancer. Alphal-2FucT DNA is useful in gene therapy and antisense therapy. The present sequence is rat hepatoma H35 cell alphal-2FucT catalytic domain.
                                                                                                                                                                                                                                                                                                        185
                                                                                                                                                                                                                                                                                                                                                             245
                                                                                                                                                                                                                                                                                                                                                                                                                  305
                                                                                                                                                                                                                                                                                                                    300
                                                                                                                                                                                                                                                GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 125
                                                                                                                                                                                                                                                                           GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120
                                                                                                                                                                 Gaps
                                                                                                                                                                                          LQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM 65
                                                                                                                                                                                                                                                                                                                                                                          1 LQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM
                                                                                                                                                                                                                                                                                                                                                                                                                RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF
                                                                                                                                                                                                                                                                                                                                                                                                                                 YRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFV
                                                                                                                                                                                                                                                                                                                                                           186 GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS
                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKVFKPEAAFLPEWVGIPADLSPLLKALTPACPRSHFHLKAKGVTCYVAGRAF 358
                                                                                                                                     Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Secretor: glycosyltransferase; FUT2; pig; epitope; antige
transgenic animal; xenotransplantation; organ transplant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1..4
/note= "N-terminal cytoplasmic tail"
                                                                                                                                     98.7%; Score 1896; DB 23;
100.0%; Pred. No. 1.3e-198;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Asn is N-glycosylated'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "C-terminal domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Porcine secretor transferase (FUT2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW37855 standard; Protein; 340 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "C
185..187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "A
251..253
                                                                                                                                                Best Local Similarity 100.
Matches 353; Conservative
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305..307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27..340
                                                                                                           353 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-FEB-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sus scrofa
                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW37855;
                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
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                                                                                                                                                                                                                                                                                                    126
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                                                                                                                                                                                                                                                                                                                                                                                                                  246
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8×3555555×8
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                                                                                                                                                                                                                                                                                                    Q \underline{\gamma}
                                                                                                                                                                                                                                                                                                                                                           Q\overline{Q}
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This polypeptide comprises porcine secretor glycosyltransferase (SE or FUT2), a type II integral membrane protein has high affinity of the type I and type III substrates. Its amino acid sequence was deduced from the nucleotide sequence of a genomic DNA clone (see AAV29003) isolated from a pig liver library on the basis of homology to human FUT2 cDNA. Pig FUT2 shows 83.2% identity with human FUT2. Expression of a glycosyltransferase, such as porcine Se, in a tissue results in reduced expression of unwanted carbohydrate pancreas, rendering if more suitable for transplantation, i.e. less immunogenic and of increased immunological acceptability. A claimed method of producing a cell from a donor species that is immunogenic and of increased immunological acceptability. A claimed method of producing a cell from a donor species that is immunologically acceptable to a recipient species involves reducing levels of carbohydrate on the donor cell that causes it to be recognised as non-self by the recipient by expressing a nucleic acid for a glycosyltransferase such as porcine Se in the cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKBFTLHDHVRBEAQAFLRGLRVN3SQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 STITHLOORIVKLOPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14:
                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid encoding glycosyltransferase able to compete with second such enzyme - particularly used to reduce expression of unwanted carbohydrate epitope(s) on tissues intended for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.5%; Score 1451; DB 19;
81.9%; Pred. No. 6.8e-150;
live 26; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339
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                               97WO-AU00540.
                                                                                           96AU-0001823.
                                                                                                                                                                                                                                Sandrin MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 81.99 Matches 271; Conservative
                                                                                                                                                             (AUST-) AUSTIN RES INST
                                                                                                                                                                                                                                                                                            WPI; 1998-169148/15.
N-PSDB; AAV29003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transplantation
                                                                                                                                                                                                                             McKenzie IFC,
                               22-AUG-1997;
                                                                                           23-AUG-1996;
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X X X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B 
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(first entry)

08-JUL-1998

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AA.
                                            AAW69332 standard; Protein; 343
                                                                                                                                                                                                                                                                                                                                               Lennon G,
                                                                                                                                                   FUT2; nonsecretor genotyping.
                                                                                                          Human Sec2 protein sequence
                                                                                                                                                                                                                                        95US-0395800
                                                                                                                                                                                                                                                            95US-0395800
                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 79.2
Matches 262; Conservative
                                                                                                                                                                                                                                                                                                                                               Kelly RJ,
                                                                                                                                                                                                                                                                                          KELLY R J.
LENNON G.
LOWE J B.
ROUQUIER S.
                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-520127/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              343 AA;
                                                                                                                                                                                                                                                                                 GIORGI D.
                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAV58323
                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                        28-FEB-1995;
                                                                                                                                                                                                                                                            28-FEB-1995;
                                                                                                                                                                                              US5807732-A.
                                                                                      20-NOV-1998
                                                                                                                                                                                                                   15-SEP-1998,
                                                                                                                                                                                                                                                                                                                                               Giorgi D,
                                                                 AAW69332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                          (KELL/)
(LENN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                (GIOR/)
                                                                                                                                                                                                                                                                                                                (LOWE/)
                                                                                                                                                                                                                                                                                                                          (ROUQ/)
                                                                                                                               Sec2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --
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                        RESULT 7
                                  AAW69332
                                                       δ
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                                                                                                                                                                                                                                                                                                                               The present sequence represents pig secretor used in an example of the present invention. The present invention describes nucleic acids (NA) encoding a chimeric glycosyltransferase. The NAs comprises a catalytic domain of a first glycosyltransferase (GT) and a localisation signal of a second GT, whereby when the NA is expressed in a cell and where the compete for substrate with a second GT, resulting in reduced levels of a product from the second GT. The NAs can be used to produce cells and organs with desired glycosylation patterns. Products and methods of the present invention can be used to reduce the levels of present invention can be used to reduce the levels of undesirable transplantation or gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSTFVGVHVRRGDYYHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding chimeric glycosyltransferases - used for altering carbohydrate levels on the surface of cells, useful in gene therapy and transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STITHLOORIVKLOPLSEKELPMTTOMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STIPHLQQRMVKIQP--TWELQMVTQVT---TESP-----SSPQLKGMWTINAIGR 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 340;
                                          chimeric; glycosyltransferase; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.5%; Score 1451; DB 19;
81.9%; Pred. No. 6.8e-150;
tive 26; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDSPFLKLFKPEAAFLPEWIGIEADLSPLLK 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 331
                                                                                                                                                                                                                                                                                                             Example 2; Fig 6; 51pp; English.
                                                                                                                                                           96US-0024279.
96AU-0001402.
                                                                                                                                       97WO-AU00492
                                                                                                                                                                                                                Sandrin MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 81.9
Matches 271; Conservative
                                                                                                                                                                                          (AUST-) AUSTIN RES INST.
                                                                                                                                                                                                                                   WPI; 1998-159170/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        340 AA;
                                                                                                                                                                                                                                                N-PSDB; AAV21639
                                                     transplantation.
                                           Pig; secretor;
                                                                                                                                                                                                                McKenzie IFC,
                                                                                                                                       01-AUG-1997;
                                                                                                                                                           21-AUG-1996;
02-AUG-1996;
                     Pig secretor
                                                                                             W09805768-A1
                                                                                                                  12-FEB-1998
                                                                         Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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\nabla Q
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This sequence is the human Sec2 protein of the invention. The DNA encodes a alpha(1,2) fluosyltransferase and is the Secretor alpha(1,2) fluosyltransferase locus, that cross hybridises with the H blood group alpha(1,2)fluosyltransferase gene. The DNA is useful for producing a recombinant human GDP-L-flucose:beta-D-galactoside 2-alpha-L-fluosyltransferase (FOT2) which can be used for genotyping an individual as a secretor or nonsecretor as it is known that nonsecretors homozygous for a mutant allele of the FOT2 gene that has a stop codon in the position corresponding to amino acid 143.
alpha(1,2) fucosyltransferase; H blood group; secretor genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WMEEETRHIPGEXVRFTGYPCSWIFYHHLRQEILQEFTLHDHVREEAAKFLRGLQVNGSR 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSTFVGVHVRRGDYVHVMPNVWRGVVADRGYLEKALDMFRARYSŠPVFVVTSNGMAWCRE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STIFHVOORLAKIOAM--WELPV------QIPVLASTSKALGPSOLRGWWTINAIGR 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         recombinant enzyme and genotyping person as secretor or nonsecretor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.3%; Score 1407.5; DB 19; Length 343; 79.2%; Pred. No. 4e-145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
                                   GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding fucosyltransferase enzyme - useful for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lowe JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Column 45-50; 55pp; English.
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12-DEC-1990;
14-FEB-1990;
14-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-FEB-1991;
                                                                                                                                                                                                                                                                                                           07-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                     WO9112340-A
                                                                                                                                                                                                                                                                                                                                                                                                                              22-AUG-1991
                                                                                                                                                                                                                                                                                   AAR13751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lowe JB;
            72
                                                                                                      192
                                                                                                                              240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is given in a specification relating to a rat ganglioside GM.1-specific alphal-2fucosyltransferase protein. The protein or its cellular fraction is useful for synthesis of a molecule comprising Fucalphal-2Galbetal-3GalNAc, a glycolipid, glycoprotein, glycolipoprotein or a free oligosaccharide comprising Fucalphal-2Galbetal-3GalNAc. The method involves contenting alphal-2fucosyltransferase with GDP-fucose and a molecule or glycolipid, glycoprotein, glycolipoprotein or oligosaccharide having a terminal Galbetal-3GalNAc group. It is also useful for synthesis of fucosyl-GM.1 by contacting the protein with GDP-fucose and ganglioside GM.1 The obtained glycoproteins, glycolipids and oligosaccharides are useful as nutritional compositions and fucosyl-GM.1 is useful for inducing an increase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New rat ganglioside GMI-specific alphal-2Fucosyltransferase, useful for preparation of fucosyl GMI which is useful as a nutritional composition or immunotherapeutic for cancer and neurological diseases -
                                                                                                                                                                                                                            neuroprotective; nootropic; gene therapy; Fucalphal-2Galbetal-3GalNAC; immunotherapy; immunosuppression; cancer; neurological disease; small cell lung carcinoma.
      NINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIXLANYTL 300
                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 STIFHVQORLAKIQAM--WELPV-----QIPVLASTSKALGPSQLRGMWIINAIGR 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 STIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunotherapeutic or immunosuppressive action against cancer, neurological disease or small cell lung carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72.7%; Score 1397; DB 21; 78.9%; Pred. No. 5.7e-144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                 PDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 331
                                                                                                                                                                                                                                                                                                                                                                                                              (PACI-) PACIFIC NORTHWEST CANCER FOUND.
                                                                                                                                    AAB36106 standard; Protein; 344 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26;
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                                                                                                                                                                                                        Human Sec2 catalytic domain
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                                                                                                                                                                                                                                                                                                                                                                                      99WO-US07384
                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Holmes EH, Sherwood AL;
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Matches 262; Conserv
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                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                               23-APR-1999;
                                                                                                                                                                                  19~FEB-2001
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                                                                                                              RESULT 8
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WMEERYRHI "PGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGS 179
                                                                                                                                                                                                                                  30 GNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMH 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The amino acid sequence codes for a protein capable of functioning as a GDP- Fuc:[beta-D-Gal alpha(1,2)- fucosyltransferase. The functional protein is represented by amino acids 33 to 365. The enzyme produced by the DNA sequence can be used in enzymatic fucosylation of chain-terminating galactose residues on lactoseamine or neolacto type beta-D-galactoside to alpha-2-L-fucose residues. See also AAR13749-R13752.
                              QPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCR
                                                                                                                                     ENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolation of gene conveying post-translational characteristic e.g. the presence of soluble or membrane bound oligo or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDP-Fuc:beta-D-galactoside alpha(1,2)-fucosyltransferase.
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63.3%; Pred. No. 4.3e-106;
ive 37; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                            LPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 331
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90US-0480133.
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LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120

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365 AA;
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                              Sequence
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                                         NALAPIFRISLPVLHSDIAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHL 149
                                                                                                                                                                                                                                                                                                              GTAMGPNASSSCPQH-PASLSGTWTVYPNGRFGNQMGQYATLLALAQLNGRRAFILPAMH 117
                                                                RPBILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA 207
                                                                                                                                                IQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDP-L-fucose-beta-D-galactoside 2-alpha-fucosyl-transferase; Fuc-T; synthesis; 2'-fucosyllactose; oligosaccharide; human milk; non-human transgenic mammal; secondary gene product.
                                                                                                                                                                                                        DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prodn. of human:ised milk by non-human transgenic mammal - by inserting heterologous gene encoding human catalytic entity which produces oligo:saccharide(s) and glyco:conjugate(s) into mammal's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDP-L-fucose-beta-D-galactosidase alpha-1,2-fucosyltransferase.
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Smith DF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA
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Prieto PA, Sm
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|PLWTLAKP 365
                                                                                                                                                                                                                                                                                                                                                                        PLLKALTP 335
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90 NALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHL 149
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                                                                                                       .68
                                                              Gaps
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                                                                                                     GNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMH
                                                                                                                                                                                                                                                                                                                                                                                                                              GDP-L-fucose-beta-D-galactoside 2-alpha-fucosyltransferase; glycosyltransferase; glycosylation; oligosaccharide; glycoprotein; glycolipid; transgenic animal; cattle; milk.
                                                                                                                                                                                                                                                                                                  150 RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFYGVHVRRGDYVHVMPNVWKGVVA
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                                                                                                                                                                                                                                                                                                                                                                                                       DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALL
            DB 16; Length 365;
                                                         73; Indels
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54.7%; Score 1051.5; DB 16
63.3%; Pred. No. 4.3e-106;
iive 37; Mismatches 73;
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                                                      Conservative
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                         Similarity
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Homo sapiens
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15-JUN-1994;
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                                                                                           Best Local Sim
Matches 195;
                                                           Seguence
                                                                                Query Match
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                                                                                                                                                                                                                                                                                  59 GTAMGPNASSSCPQH-PASLSGTWTVYPNGRFGNQMGQYATLLALAQLNGRRAFILPAMH 117
                                                                                                                                                       118 AALAPVFRITLPVLAPEVDSRTPWRELQLHDWMSEEYADLRDPFLKLSGFPCSWTFFHHL 177
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                                                                    Gaps
                                                                                     30 GNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMH 89
                                                                                                                                                                                                                          DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alpha-1,2-fucosyltransferase (AAR70421) is encoded by a cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ijυ
                                           54.7%; Score 1051.5; DB 16; Length 365; 63.3%; Pred. No. 4.3e-106; ive 37; Mismatches 73; Indels 3;
                                                                    3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDP-L-fucose-beta-D-galactoside 2-alpha-fucosyltransferase; glycosyltransferase; oligosaccharide; glycoprotein; glycolipid; transgenic animal; cattle; glycosylation; milk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transgenic animal expressing heterologous catalyst - used in metabolite prodn esp. glycosyltransferase for prodn. of oligosaccharide(s) and glyco-conjugate(s) in the milk, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'n,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mukerji
  glycosylated proteins and lipids in the milk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kopchik JJ, Moremen KW, rieto PA, Smith DF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62-64; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            AAR70421 standard; Protein; 365 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95WO-US01147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       foods, pharmaceuticals, etc,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             2-Alpha-fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                Matches 195; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prieto PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1995-328279/42.
N-PSDB; AAT01082.
                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ABBO ) ABBOTT LAB.
                       365 AA;
                                                                                                                                                                                                                                                                                                                  PLLKALTP 335
                                                                                                                                                                                                                                                                                                                                        PLWTLAKP 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                        27-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9524488-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cummings RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-SEP-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pierce JM,
                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                  AAR70421;
                                           Query Match
                                                       Best Local
                                                                                                                                                                                                                          208
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SXSS
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90 NALAPIFRISLPYLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHL 149
                                                                                                                                                                                          59 GTAMGPNASSSCPQH-PASLSGTWTVYPNGRFGNQMGQYATLLALAQLNGRRAFILPAMH 117
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                 RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA 207
                                                                                                                                                                                                                                                                                                                                                            DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALL 267
                                                                                                                                                                                                                                                                                                                                                                                                                         TQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS 327
                                                                                                                                                                                                                                                                                                                                                                                                                                        30 GNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMH 89
(AAT01082) isolated from a human epidermal carcinoma cell line A431 cDNA library. The enzyme can be expressed in the milk of a transgenic mammal, esp. cow. This allows large-scale prodn. of oligosaccharides or glycosylated proteins and lipids in the milk.
                                                                                                                                                                                                                                                                                                                                                                              Redn. of rejection of xenogeneic cells following transplantation by introducing a vector expressing fucosyl:transferase into the cells
                                                                                                                                             ..
m
                                                                                                             DB 16; Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H-transferase; xenograft hyperacute rejection; transplantation; glycosyltransferase; galactose alpha(1,3) galactose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sandrin MS, Squinto SP;
                                                                                                                                           73; Indels
                                                                                                          54.7%; Score 1051.5; DB 16
63.3%; Pred. No. 4.3e-106;
iive 37; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rother RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 45-47; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein; 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94US-0278282.
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                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ALEX-) ALEXION PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fodor WL, Mckenzie IFC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AUST-) AUSTIN RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human H-transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-049326/05
                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR90572 standard;
                                                                              365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLLKALTP 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLWILAKP 365
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3
                                                                                                                                                                                                                                                              90 NALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHL 149
             The human H-transferase (AAR90572) product of a cDNA clone (AAT12238) prepd. from human epidermoid carcinoma cells (ATGC CRL 155 A-431) can be expressed in xenogeneic organs, tissues and cells using a vector such as pAPEX-1 (AAT12239). This results in decreased expression of the non-human antigen galactose alpha(1,3) galactose reduced upon transplantation to humans.
                                                                                                                                                                                                                                                                                     AALAPVFRITLPVLAPEVDSRTPWRELQLHDWMSEEYADLRDPFLKLSGFPCSWTFFHHL 177
                                                                                                                                                                                                                                                                                                                       150 RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA 207
                                                                                                                                                                                                                                                                                                                                       DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALL 267
                                                                                                                                                                                                                                                                                                                                                                                             TQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                     59 GTAMGPNASSSCPQH-PASLSGTWTVYPNGRFGNQMGQYATLLALAQLNGRRAFILPAMH 117
                                                                                                                                                                                                           30 GNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMH 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human GDP-L-fucose:beta-D-galactoside-2-alpha-L-fucosyltransferase;
                                                                                                                                                                                   m
                                                                                                                                                         Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alpha 1,2 FT; transgene; transgenic mouse; animal model; intestinal adhesion; Helicobacter pylori infection; stomach; small intestine; gut; epithelial cell; surface receptor; carbohydrate antigen; gastritis; peptic ulcer; neoplasia; gastric adenocarcinoma; Lewis antigen; fucosylation.
                                                                                                                                                                                  73; Indels
                                                                                                                                                       DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human alpha 1,2 fucosyltransferase (EC 2.4.1.69).
                                                                                                                                                      Score 1051.5; DB 17
Pred. No. 4.3e-106;
7; Mismatches 73;
                                                                                                                                                                               37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW23805 standard; Protein; 365
                                                                                                                                                      54.78;
63.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                  Conservative
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N-PSDB; AAT76768.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gordon JI;
                                                                                                                                                  Query Match
Best Local Similarity
Matches 195; Conserv
                                                                                                                          365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLLKALTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLWTLAKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US5625124-A.
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                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW23805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Falk P,
                                                                                                                                                                                                                                                                                           118
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ells, the enzyme human GDP-Livose:beta-D-galactoside 2-alpha-L-fucosyltransferase (also called alpha 1,2 FT) or human GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase (also called alpha 1,2 FT) or human GDP-L-fucose: beta-D-N-acetylglucosamide 3/4-alpha-L-fucosyltransferase (also called alpha 1,3/4 FT). The enzyme is expressed under the control of agut epithelial cell-specific promoter and Helicobacter pylori adhers to the transgenic cells. The transgenic mouse and intestinal epithelial cells from it are useful as models for screening compounds for the ability to inhibit adhesion of H. pylori to gut and was published by Larsen et al., Proc.Natl.Acad.Sci.USA, 87: 6674-6678 (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207
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                                                                                                                                                                                                                                                                                                                                                                                                                                               90 NALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMBERYRHIPGHFVRFTGYPCSWTFYHHL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237
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                                                                                                    epitheliai
                                                                                                                                                                                                                                                                                                                                                                                                          150 RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA
                                                                                                                                                                                                                                                                                                                                                                                      30 GNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSAYLRQAMDWFRARHEAPVFVVTSNGMEWCKENIDTSQGDVTFAGDGQEATPWKDFALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWGIPADLS
                                                                                                                                                                                                                                                                                                                               DB 18; Length 365;
             Helicobacter pylori infection - comprising expressing human enzyme promoting intestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alpha(1,2)-fucosyltransferase; glycosylation; oligosaccharide;
                                                                                                                                                                                                                                                                                                                                                             73; Indels
                                                                                                   A claimed transgenic mouse expresses, in its intestinal
                                                                                                                                                                                                                                                                                                                           54.7%; Score 1051.5; DB 18 63.3%; Pred. No. 4.3e-106;
                                                                                                                                                                                                                                                                                                                                                        37; Mismatches
                                                                    Example 1; Columns 13-16; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human alpha(1,2)-fucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW13640 standard; Protein; 365 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-US13816
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                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                               365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        328 PLLKALIP 335
                           ransgenic mouse
             Animal model for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLWTLAKP
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                                                                                                                                                                                                                                                                                                                                                       195;
                                                                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                        Matches
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Пp
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Human GDP-Fuc:beta-D-galactoside alpha(1,2)-fucosyltransferase (AAW13640) is an enzyme involved in the expression of type I and II blood group is tructures. Its amino acid sequence was deduced from an isolated DNA (AAT61677) derived from human A431 cells. Expression of the fucosyltransferase animal cell lines provides specific capabilities with respect to post-translational modification of the oligosaccharides of expressed proteins or lipids. Specific applas. Of the enzyme include enzymatic fucosylation of chain-terminating galactose residues on lactoseamine or neolacto type beta-D-galactoside to alpha-2-fucose residues. The enzyme can also be used to raise antibodies as diagnostic reagents and to screen cpds. for fucosyltransferase inhibitor activity.
                                                                                                                                                     New recombinant fucosyltransferase proteins - useful for modifying cell surface oligosaccharide structures
                                                                                                                                                                                                               Example 1; Page 280-281; 329pp; English.
                (UNMI ) UNIV MICHIGAN.
                                                         Lowe JB;
                                                                                          WPI; 1997-192897/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               365 AA;
                                                                                                                N-PSDB; AAT61677
                                                     Legault DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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90 NALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERXRHIPGHFVRFTGYPCSWTFYHHL 149 59 GTAMGPNASSSCPQH-PASLSGTWTVYPNGRFGNQMGQYATLLALAQLNGRRAFILPAMH 117 150 RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA 207 DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALL 267 30 GNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMH 89 / Match 54.7%; Score 1051.5; DB 18; Length 365; Local Similarity 63.3%; Pred, No. 4.3e-106; nes 195; Conservative 37; Mismatches 73; Indels 3; Best Loca Matches 208 qq δž g ÓΫ q Qy

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268 TOCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWYGIPADLS 327

QQ ΩY Db 328 PLLKALTP 335

PLWTLAKP 365

Search completed: May 27, 2003, 15:06:15 Job time : 46.4049 secs

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APP1
APP11
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Appli
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                                                                                                                                                 (without alignments) 715.625 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12
Sequence 13
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                                                                                                           TITLE OF INVENTION: UNCLEIC ACIDS AND PROTEINS OF A RAT CANGLIOSIDE TITLE OF INVENTION: GMI-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERASE AND USES TITLE OF INVENTION: THEREOF FILE REPERENCE: 8511-029
CURRENT APPLICATION NUMBER: US/09/298,886
CURRENT PILING DAIE: 1999-04-26
NUMBER OF SEQ ID NOS: 29
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Pred. No. 8.7e-214;
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Mismatches
                                     Sequence 8, Application US/09298886
Patent No. 6329170
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                                                                            GENERAL INFORMATION:
APPLICANT: Eric H. Holmes et al
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US-09-298-886-8
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Best Local Similarity
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RESULT 1
US-09-298-886-8
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        Sequence 10, Application US/0929886
Patent No. 6329170
GENERAL INFORMATION
TITLE OF INVENTION: MUCLEIC ACIDS AND PROTEINS OF A RAT GANGLICSIDE
TITLE OF INVENTION: MUCLEIC ACIDS AND PROTEINS OF A RAT GANGLICSIDE
TITLE OF INVENTION: MUCLEIC ALPHA1-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 29
SOFTWARE PATENTICH VOY: 2.0
SEQ ID NO 10
LENGTH: 353
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APPLICANT: SANDRIN, MAURO S.
APPLICANT: SANDRIN, MAURO S.
APPLICANT: SANDRIN, MAURO S.
TITLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
FILE REFERENCE: 30562.50SWO
CORRENT PAPLICATION NUMBER: 0S/09/254,077A
CURRENT FILING DATE: 1999-061.
PRIOR FILING DATE: 1999-08-22
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
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Pred. No. 2e-159;
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al Similarity 100.0%; Pred. No. 6.1
353; Conservative 0; Mismatches
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81.9%;
                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Rattus norvegicus
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Best Local Similarity
US-09-298-886-10
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Matches 35
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249 NINASRGDVVFAGNGIEGSPAKDFALLIQCNHTVMTIGTFGIMAAYLAGGETIXLANYTL 308
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                                                                                                                                        LGNOMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWONYHLND 120
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    Gaps
                                               STITHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR 60
                                                                                 STIFHLQQRMVKIQP--TWELQMVTQVT---TESP-----SSPQLKGMWTINAIGR 68
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APPLICANT: MCKENZIE, IAN C. F.
TITLE OF INVENTION: NUCLERC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
FILE REFERENCE: 30562.5049
CURRENT FILING DATE: 1999-06-11
PRIOR PILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: PO 1823
PRIOR FILING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATCHIN VOI. 2.1
SEQ ID NO.?
: P:
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81.9%; Pred. No. 2e-159;
Live 26; Mismatches 2
  Mismatches
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26;
  Conservative
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US-09-254-077A-7
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61 LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
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TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAT CANGLIOSIDE
TITLE OF INVENTION: GML-SPECIFIC ALPHA1-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 8511-029
CURRENT APPLICATION NUMBER: US/09/298,886
CURRENT APPLICATION NUMBER: US/09/298,886
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: SANDEIN, MAURO S.
APPLICANT: AMCKNIZIAN C. F.
TILLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
FILE REFERENCE: 30562.50SN0
CURRENT APPLICATION NUMBER: 105/99/254,077A
CURRENT ELLING DAIE: 1999-06-11
PRIOR FILLING DAIE: 1997-08-22
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                                     PDSPFLKIFKPEAAFLPEWTGIAADLSPLLK 342
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PDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 331
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                                                                                                                                             Sequence 8, Application US/09254077A Patent No. 6399758
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PRIOR FILING DATE: 1996-08-23
NUMBER OF SEO ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
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US-09-254-077A-8
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2-ALDHA-L-FUCOSYLIRANSFERASES, DNA SEQUENCES ENCODING THE
2-ARE, METHOD FOR PRODUCING THE SAME AND A METHOD OF
GENOTYPING A PERSON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HICHWAY, SUITE 400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM FC Compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                          309 POSPFLKLFKPEAAFLPEWIGIEADLSPLLK 339
                 PDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, V. CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/395,800A
                                                                                                                                                               Sequence 8, Application US/08395800A
Patent No. 5807732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                     APPLICANT: ROUQUIER, SYLVIE
APPLICANT: GIORGI, DOMINIQUE
APPLICANT: KELLY, ROBERT J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-220
TELEX: 24885 OPAT UR
INFORMATION FOR SO ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: LOWE, JOHN B
APPLICANT: LENNON, GREGORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 28-FEB-1995
CLASSIFICATION: 435
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amino acid
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Best Local Similarity 79.29
Matches 262; Conservative
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                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: G
TITLE OF INVENTION: 2
TITLE OF INVENTION: S
TITLE OF INVENTION: G
NUMBER OF SEQUENCES:
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: USA
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US-08-395-800A-8
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Score 1086; DB
Pred. No. 4.5e-
0; Mismatches
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; Sequence 11, Application PC/TUS9100899
; GENERAL INFORMATION:
; APPLICANT: LOWE, John B.
                                                                                                                                                                                                Sequence 12, Application US/09254077A Patent No. 6399758
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58.7%;
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Best Local Simi
Matches 206;
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                                                                                                                                                                                  121 WMEERYRHI-PGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGS 179
                                                                                                                                                                                                                                              180 QPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCR 239
                                                                                                                                                                                                                                                                                                       ENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYT 299
                                                                                                                                                                  61 LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
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                                                                                                                          23 STIFHVQQRLAKIQAM--WELPV-----QIPVLASTSKALGPSQLRGMWTINAIGR 71
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APPLICANT: SANDELN, MAURO S.
APPLICANT: SANDELN, MAURO S.
TITLE ON TOWNERS OF THE SANDELN, MAURO S.
TITLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
FILE REFERENCE: 30562.5USWO
CURRENT APPLICATION NUMBER: US/09/254,077A
CURRENT FILING DATE: 1999-06-11
PRIOR PILING DATE: 1997-08-22
PRIOR FILING DATE: 1997-08-23
PRIOR FILING DATE: 1996-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 STITHLOORIVKLOPLSEKELPMTTOMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR
                                                                                                        STIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR
                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.7%; Score 1396.5; DB 4; Length 347; 79.2%; Pred. No. 4.3e-153;
                                            Length 344;
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                                                                            Indels
                                            72.7%; Score 1397; DB 4; 78.9%; Pred. No. 3.7e-153;
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                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              300 LPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/09254077A Patent No. 6399758
                                                                          26;
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SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262; Conservative
                                                                          Conservative
; ORGANISM: Homo sapiens US-09-298-886-11
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                                                            Similarity
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                                                                          262;
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Matches
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TITLE OF INVENTION: Wethod and Products For the synthesis of Synthesis of TITLE OF INVENTION: Oligosaccharide Structures on Glycoprotedins, Glycolipids, TITLE OF INVENTION: or as Free Molecules, and For the Isolation of Cloned TITLE OF INVENTION: Genetic Sequences That Determine These Structur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188
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                                                                                                                              NINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTL 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SANDKIN, MAURO S.
APPLICANT: ANCENZIE, IAN C. F.
TITLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
FILE REPERENCE: 30562.50000
CURRENT APPLICATION NUMBER: 05/09/254,077A
CURRENT PILING DATE: 1999-06-11
PRIOR PELICATION NUMBER: PCT/A097/00540
PRIOR PELICATION NUMBER: PCT/A097/00540
PRIOR PELICATION NUMBER: PO 1823
PRIOR FILING DATE: 1997-08-23
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249 FRARHEAPIFVVTSNGMKWCWENIDASRGDVVFAGNGLESSPAKDFALLTQCNHTVMTIG
23 SFLLHLHODLFRNGLALSLPCLEROPVPAPVAIVCLPVTSPASNASSCAGRPAAPS----
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4.5e-117;
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METHODS AND PRODUCTS FOR THE SYNTHESIS
OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISCLATION
OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90 NALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHL 149
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                                                                                                                ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/914,281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.7%; Score 1051.5; DB 1 63.3%; Pred. No. 4.3e-113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2363-060-55
                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Lavallaye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-066
                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-393-246-6
; Sequence 6, Application US/08393246
; Patent No. 5595900
; Patent INFORMATION:
GENERAL INFORMATION:
APPLICANT: LOWE, JOHN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (703)521-4500
                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 365 amino acids
AMINO ACID
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-07-914-281-6
                                                                                             CORRESPONDENCE ADDRESS
  TITLE OF INVENTION: DITTE OF INVENTION: GITTE OF INVENTION: GITTE OF INVENTION: GNOBER OF SEQUENCES:
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                                                                                                                                                                                               Virginia
(: U.S.A.
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Best Local Similarity
Matches 195; Conserv
                                                                                                                                                                           CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             328 PLLKALTP 335
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                                    :: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
:: P.C.
1755 Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US91/00899
FILING DATE: 19910214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73;
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Fred. No. 3.7e-113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37; Mismatches
                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye Ph.D., Jean-Paul
REGISTRATION NOMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-021-55 PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-5940
TELEPAX: (703)486-2347
TELEPX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                  PC-DOS/MS-DOS
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; Sequence 6, Application US/07914281
: Patent No. 5324663
; GENERAL INFORMATION:
                                                                                                                                                                     MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 333 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C-terminal
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                                                                                                                                                         COMPUTER READABLE FORM:
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                  CORRESPONDENCE ADDRESS
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: YES FRAGMENT TYPE: C-t ORIGINAL SOURCE:
                                                                                         CITY: Arlington
STATE: Virginia
ZIP: 22202
                                                                                                                                                                                                                                                                                       FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo
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                                    ADDRESSEE:
ADDRESSEE:
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                                                                           STREET:
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Sequence 1, Application US/08273411
Patent No. 5655124
GENERAL INFORMATION:
APPLICANT: Falk, Per
APPLICANT: Gordon, Jeffrey I.
ITTLE OF INVENTION: Animal Model for TITLE OF INVENTION: Disease
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: WU
TELECOMMUNICATION INFORMATION:
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Proc. Nat'l Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (404) 815-6508
TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           365 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 195; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1.365
OTHER INFORMATION: /n.
PUBLICATION INFORMATION:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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STRANDEDNESS: si
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                                                                                                                                                                                                                                                       Georgia
                                                                                                                                                                                                                                   Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                   STATE: GOUNTRY:
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                   OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS, GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 GIAMGPNASSSCPQH-PASLSGTWTVYPNGRFGNQMGQYATILALAQLNGRRAFILPAMH 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150 RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 365;
                                                                                                                 OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT P.C.
                                                                                                                                                     F: 1755 Jefferson Davis Highway, Fourth Floor Arlington
                                                                                                                                                                                                                                                                                                            YSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.7%; Score 1051.5; DB 1; 63.3%; Pred. No. 4.3e-113; Live 37; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 2363-060-55 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/220,433
FILING DATE: 30-MR-199
APPLICATION NUMBER: US 07/914,281
FILING DATE: 20-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: LAVALIESE, JGAN-FBUIL P.
REGISTRATION NUMBER: 31,451
                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,246
                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 6:
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                                                                                               CORRESPONDENCE ADDRESS:
TITLE OF INVENTION: MITITE OF INVENTION: OI TITLE OF INVENTION: OI TITLE OF INVENTION: OI NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                             Virginia
: U.S.A.
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Best Local Similarity
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                                                                                                                 ADDRESSEE:
ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                SOFTWARE
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RESULT 13

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/note= "GDP-L-fucose:beta-D-Galactoside-2-alpha-L-fucosyl
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for Gastro-Intestinal
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                                                                                                                                                                                                                                                                                                         54.7%; Score 1051.5; DB 1
63.3%; Pred. No. 4.3e-113;
tive 37; Mismatches 73;
                                                                                       :: Patrea L. Pabst
1100 Peachtree Street, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208
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GDP-L-FUCOSE: BETA-D-GALACTOSIDE
2-ALPHA-L-FUCOSYLITRANSFERASES, DNA SEQUENCES ENCODING THE
SAME, METHOD FOR PRODUCING THE SAME AND A METHOD OF
GENOTYPING A PERSON
                                               298 TQCNHIIMTIGTEGEWAAYLAGGDTVYLANFTLPDSBFLKIFKPEAAFLPEWVGINADLS 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90 NALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHL 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.30
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28-FEB-1995
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                                                                                                                                                                                                                                                Sequence 6, Application US/08395800A Patent No. 5807732
                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: LOWE, JOHN B
APPLICANT: LENNON, GREGORY
APPLICANT: ROUGUIER, SYLVIE
APPLICANT: GLORI, DOMINIQUE
APPLICANT: GLORI, BOBERT
ITILE OF INVENTION: GDP-L-FUCOS
TITLE OF INVENTION: SAME, METHC
ITILE OF INVENTION: GRANE, METHC
ITILE OF INVENTION: GENOIYPING
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (703) 413-3000
(703) 413-2220
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LLEY: ARLINGTON
STATE: VIP
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Best Local Similarity
                                                                                                         PLLKALTP 335
                                                                                                                                                358 PLWTLAKP 365
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TELEFAX: (
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                                                                                                         328
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                                                                                                                                                                                                                                                                                                                         LOWE, JOHN B.
FENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
FENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
FENTION: GLYCOLIFIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
FENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
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                                                            238 DSAYLRQAMDWFRARHEAPVFVVTSNGMEWCKENIDTSQGDVTFAGDGQEATPWKDFALL
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1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 365;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,058A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.7%; Score 1051.5; DB 1
63.3%; Pred. No. 4.3e-113;
tive 37; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                    Sequence 6, Application US/08525058A
Patent No. 5770420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMONICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEX: 248855 OPAT INFORMATION FOR SEQ ID NO: 6:
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amino acid
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Best Local Similarity 63.3%
Matches 195; Conservative
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                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: MI
TITLE OF INVENTION: GI
TITLE OF INVENTION: GI
TITLE OF INVENTION: GI
NUMBER OF SEQUENCES:
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3. /gqn2_6/ptodata/2/pubpa/PCT_NEW_PUB.pep:*

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5. /gqn2_6/ptodata/2/pubpa/USO7_NEW_PUB.pep:*

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7. /gqn2_6/ptodata/2/pubpa/USO7_NEW_PUB.pep:*

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10. /gqn2_6/ptodata/2/pubpa/USO9_PUBCOMB.pep:*

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14. /gqn2_6/ptodata/2/pubpa/USO0_NEW_PUB.pep:*
GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	Sequence 8, Appli Sequence 8, Appli Sequence 10, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 25, Appli Sequence 25, Appli Sequence 27, Appli Sequence 27, Appli Sequence 29, Appli Sequence 29, Appli Sequence 29, Appli Sequence 29, Appli Sequence 29, Appli Sequence 29, Appli Sequence 647, Appli Sequence 647, Appli Sequence 647, Appli Sequence 10, Appli
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ALIGNMENTS

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Sequence 8, Application US/0999672;
Sequence 8, Application US/0999672;
Patent No. US2002012/655A1
GENERAL INFORMATION:
APPLICANT: EIL H. HOLMES et al.
TITLE OF INVENTION: MAI-SPECIFIC ALPHAL-2 FUCOSYLTRANSFERASE AND USES;
TITLE OF INVENTION: THEREOF;
FILE REFRENCE: 8511-029
CURRENT APPLICATION NUMBER: US/09/999,672
CURRENT FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: US/09/298,886
PRIOR FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 29
SOOTWARRE: PATENTIN VEY: 2.0
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Best Local Similarity 100.0%; Pred. No. 1.7e-190;
Matches 358; Conservative 0; Mismatches 0;
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RESULT 1
US-09-999-672-8
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PRIOR FILING DATE: 1999-04-26
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241 NINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGFFGIWAAYLAGGDTIYLANYTL 300
                    NINASRGDVVFAGNGIEGSPAKDFALLIQCNFTIMTIGTFGIWAAYLAGGDTIYLANYTL 322
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Sequence 10, Application US/09999672

Sequence 10, Application US/09999672

Sequence 10, Application US/0999672

GENERAL INFORMATION:

APPLICANT: Eric H. Holmes et al.

TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE

TITLE OF INVENTION: GM1-SPECIFIC ALPHA1-2 FUCOSYLTRANSFERASE AND USES

TITLE OF INVENTION: THRREOF

FILE REFERENCE: 8511-029
                                                                                                                                                                                                                                          APPLICANT: Eric H. Holmes et al.
TITLE OF INVENTION: UNCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE
TITLE OF INVENTION: GM.-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: 8311-029
CURRENT APPLICATION UNMBER: US/10/040,863
CURRENT APPLICATION NUMBER: US/10/1011-01
PRIOR APPLICATION NUMBER: 09/298,886
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 29
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                                                                    PDSPFLKVFKPEAAFLPEWVGIPADLSPLLKALTPACPRSHFHLKAKGVTCYVAGRAF 358
                                                                                     PDSPELKVEKPEAPELPEWVGIPADLSPLLKALIPACPRSHFHLKAKGVTCYVAGRAF
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Pred. No. 1.7e-190;
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                                                                                                                                                                                           Sequence 8, Application US/10040863
Patent No. US20020137165A1
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100.0%;
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Matches 358;
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APPLICANT: Eric H. Holmes et al.

APPLICANT: Eric H. Holmes et al.

TITLE OF INVENTION: MUCLEDE ACIDS AND PROTEINS OF A RAT GANGLIOSIDE
TITLE OF INVENTION: GAL-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENTION: THREOF
FILE REFERENCE: 8511-029
CURRENT APPLICATION NUMBER: US/10/040,863
CURRENT FILING DATE: 2001-11-01
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                         GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 125
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                                                                                                                                                                                                               Score 1896; DB 10;
Pred. No. 5.8e-188;
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100.0%; Pred. No. 5.8e~188;
ive 0; Mismatches 0;
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Best Local Similarity 100.0%; P.
Matches 353; Conservative 0;
                                                                                                                                  ; ORGANISM: Rattus norvegicus
US-09-999-672-10
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US-10-040-863-10
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NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver.
SEQ ID NO 10
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US-10-040-863-11
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APPLICANT: MCKENZIE, IAN FARQUHAR CAMPBELL
APPLICANT: ACKENZIE, IAN FARQUHAR CAMPBELL
TITLE OF INVENTION: MAURO SERGIO
FILLE OF INVENTION: GLYCOSYLTRANSFERASE
FILE REFERENCE: 30562.60SWO
CURRENT APPLICATION NUMBER: US/09/051,034A
CURRENT FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/024,279
PRIOR FILING DATE: 1996-08-21
PRIOR APPLICATION NUMBER: 60/024,279
PRIOR FILING DATE: 1996-08-21
PRIOR FILING DATE: 1996-08-21
PRIOR FILING DATE: 1996-08-21
PRIOR FILING DATE: 1996-08-21
SPRIOR FILING DATE: 1996-08-21
SPRIOR FILING DATE: 1996-08-21
SPRIOR FILING DATE: 1996-08-21
SOFTWARE: PALENTIN NUMBER: PO1402
NUMBER OF SEQ ID NOS: 14.
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                                                                                                                                                                                      306 LKVFKPEAAFLPEWVGIPADLSPLLKALTPACPRSHFHLKAKGVTCYVAGRAF 358
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81.9%; Pred. No. 6.9e-142;
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US-09-051-034A-2
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Best Local Similarity
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US-09-051-034A-2
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RESULT 6 US-09-999-672-11

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APPLICANT: Exic H. Holmes et al.

TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE
TITLE OF INVENTION: GMI-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERAŜE AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 8511-029
CURRENT APPLICATION NUMBER: US/09/999,672
CURRENT FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: US/09/298,886
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Patent No. US20020137165A1

GENERAL INFORMATION:
APPLICANT: Eric H. Holmes et al.
TITLE OF INVENTION: GMI-SPECIFIC ALPHAI-2 FUGOSYLTRANSFERASE AND USES
TITLE OF INVENTION: THERROF
FILE REPERENCE: 8511-091
CURRENT APPLICATION NUMBER: US/10/040,863
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Pred. No. 2.8e-136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 72.7%; Score 1397; DB 10; Best Local Similarity 78.9%; Pred. No. 2.8e-136; Matches 262; Conservative 26; Mismatches 32;
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PRIOR FILING DATE: 1999-04-23
NUMBER: OF SQ ID NOS: 29
SOPTWARD.
Sequence 11, Application US/09999672 Patent No. US20020127655A1
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78.9%;
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SOFTWARE: PatentIn Ver. 2.0
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SEQ ID NO 11
LENGTH: 344
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US-09-672-11
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Best Local Similarity
                                                  GENERAL INFORMATION:
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TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
OF OLIGOSACCHARLES STRUCTURES ON GLYCOPROTEINS,
GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 GTAMGPNASSSCPQH-PASLSGTWTVYPNGRFGNQMGQYATLLALALAQLNGRRAFILDAMH 117
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30 GNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMH 89
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                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10; Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.7%; Score 1051.5; DB 1
63.3%; Pred. No. 1.9e-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/863,475A FILING DATE: 24-may-2001 CLASSIFICATION: <UNKnown>PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 07/914,281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Lavalleye, Jean-Paul M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 20-JUL-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
                                                                                                                                                                                                      Sequence 6, Application US/09863475A Patent No. US20020102688A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                     APPLICANT: LOWE, JOHN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22202
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                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                        PLLKALTP 335
                                                                                                    PLWILAKP 365
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Publication No. US20030068818A1
GENERAL INFORMATION:
CAPERAL INFORMATION:
CAPPLICANT: Geron Corporation
APPLICANT: Geron Corporation
APPLICANT: Clark, A. John
TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Compatible for Human
TITLE OF INVENTION: Transplantation and a Carbohydrate Determinant Selection System
FILE OF INVENTION: Recombination
FILE REPERENCE: 731/002
CURRENT APPLICATION NUMBER: US/10/105,963
CURRENT FILING DATE: 2002-03-21
PRIOR FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                         ENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYT 299
                                                                                                                                                                                                                                                                                                                                                                                               121 WMEERYRHI-PGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGS 179
                                                                                                                                                                                                                                  QPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCR 239
                                                                                                                                                                                                                                                                                                              LGNOMGEYATLFALARMNGREAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
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                                         STITHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR 60
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12;
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  Indels
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32;
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    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 LPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 331
26;
                                                                                STIFHVQQRLAKIQAM~~WELPV---
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    Conservative
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SOFTWARE: Patentin versic
SEQ ID NO 10
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ORGANISM: Homo sapiens
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US-10-105-963-10
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ORGANISM: Porcine
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Best Local Simi
Matches 194;
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US-09-844-705-13
                                                                                                                                                                                                                                                                                                                            US-09-844-268-13
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Matches 194;
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                                                                     TQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS 327
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                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09051034A

Patent No. US20010055584A1

GENERAL INFORMATION:
APPLICANT: MCKERZIE, IAN FARQUHAR CAMPBELL
APPLICANT: SANDRIN, MAURO SERGIO
TILLE OF INVENTION: IMPROVED NUCLEIC ACIDS ENCODING A CHIMERIC
TILLE OF INVENTION: IMPROVED NUCLEIC ACIDS ENCODING A CHIMERIC
TILLE OF INVENTION: IMPROVED NUCLEIC ACIDS ENCODING A CHIMERIC
TILLE OF INVENTION: IMPROVED NUCLEIC ACIDS
CURRENT APPLICATION NUMBER: US/09/051,034A
CURRENT FILING DATE: 1998-03-31
PRIOR PPLICATION NUMBER: ECT/AU97/00492
PRIOR PPLICATION NUMBER: 60/024,279
PRIOR PPLING DATE: 1996-08-21
PRIOR PPLING DATE: 1996-08-21
PRIOR PLING DATE: 1996-08-21
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62.6%; Pred. No. 6.2e-100;
Mismatches 75; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                              PLLKALTP 335
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                                                                                                                                                                                                                                                                            RESULT 10
US-09-051-034A-4
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TITLE OF INVENTION: METHODS AND COMPOSITIONS TO IDENTIFY SWINE GENETICALLY TITLE OF INVENTION: METHODS AND COMPOSITIONS TO IDENTIFY SWINE GENETICALLY TITLE OF INVENTION: RESISTANT TO F18 E. COLI ASSOCIATED DISEASES FILE REFERENCE: 21419/90368
CURRENT APPLICATION NUMBER: US/09/844,268
CURRENT FILING DATE: 2001.04-27
PRIOR APPLICATION NUMBER: 09/443,766
PRIOR FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATCHIN VEF. 2.0
SEQ ID NO 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMP 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 NVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGS 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEW 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 PMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRL 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 PMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRL 81
                                                                                                                                                                                                                                                                                                                                                                                                     Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.4%: Score 1044.5; DB 10; Lengt 62.6%; Pred. No. 1e-99; vative 38; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: VOGELI, PETER
TITLE OF INVENTION: METHODS AND COMPOSITIONS TO IDENTIFY
TITLE OF INVENTION: RESISTANT TO F18 E. COLI ASSOCIATED
FILE REPERENCE: 21419/90368
CURRENT APPLICATION NUMBER: US/09/844,705
CURRENT APPLICATION TOWNER: 09/443,766
PRIOR APPLICATION TWERE: 09/443,766
PRIOR FILING DATE: 1999-11-19
                                                                                                                                                                                                                                                                                                                                                                                                     DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      75;
                                                                                                                                                                                                                                                                                                                                                                                                     54.4%; Score 1044.5; Di 62.6%; Pred. No. 1e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/09844705
Patent No. US20020138386A1
GENERAL INFORMATION:
APPLICANT: BOSWORTH, BRAD
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SOFTWARE: Patentin Ver. 2.0
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350 VGINADLSPL 359
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RESULT 15
US-09-479-614-14
Sequence 14, Application US/09479614
Publication No. US20030013183A1
GENERAL INFORMATION:
                                                                          US-10-214-524-25; Sequence 25, Application US/10214524; Publication No. US20030073142A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 5.2%;
Best Local Similarity 25.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Cat (Felis catus) US-10-214-524-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 25.04
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55; Conservative
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  276 HENJICKEWVKI--
                                                                                                                                        GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226 DKEEEAYWDMLLMQSCKHGIIANSTYSWWAAXL------MEN---PEKIIIGPKHWLFG 275
51 PVAIFCLAGIPVHPNASDSCPKH-PASFSGTWTIYPDGRFGNQMGQYATLLALAQLNGRQ 109
                                     82 AFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPC 141
                                                                        110 АГІОРАМНАУLAPVFRITLPVLAPEVDRHAPWRELELHDWMSEDYAHLKEPWLKLTGFPC 169
                                                                                                                    SWIFYHHLRPEILKEFILHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMP 199
                                                                                                                                                                                              NVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGS 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, Ge
APPLICANT: Palcic, Monica
TITLE OF INVENTION: ALPHA 1,2-FUCOSYLTRANSFERASE
FILE REFERENCE: 07254-061002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEAAFLPEWVGIPADLSPLLKALTPACPRSHFHLKAK 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/848,838
CURRENT FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: US 09/433,598
PRIOR FILING DATE: 1999-11-02
PRIOR APPLICATION NUMBER: US 60/107,268
PRIOR FILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 23
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Patent No. US20020037570A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT; ORGANISM: Helicobacter pylori
US-09-848-838-2
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Best Local Similarity 24.09
Matches 81; Conservative
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US-09-848-838-2
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APPLICANT: WECALT.
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APPLICANT: WEALT.
APPLICANT: Feline Immunoglobulin E Molecules and Related Methods
FILE REFERENCE: P-1047
CURRENT APPLICANT: NOMBER: US/09/479,614
CURRENT APPLICANT: 2000-01-07
EARLIER APPLICANT: 1999-01-07
SERLIER FILING DATE: 1999-01-07
SOFTWARE: PATENT: NOS: 42
SOFTWARE: PATENT: NOS: 42
                                                                                                                                                                                                                             APPLICANT: Chen, Swey-Shen Alex
APPLICANT: Yang, Yong-Min
APPLICANT: Barankiewicz, Theresa J.
APPLICANT: Chen, Zhong
TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
FILE REFERENCE: IGE-00101.P.1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 RGDYVHYMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGM--AWCRENINASRGD 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 VVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSP---F 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 GHFVRFTGYPCSWIFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFVGVHVR 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 GHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFVGVHVR 190
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---ESHFEVKSQ 296
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0.14;
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CURRENT FILING DATE: 2002-08-08
PRIOR APPLICATION NUMBER: 60/312,120
PRIOR FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin version 3.1
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Pred. No. (
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Search completed: May 27, 2003, 15:25:42 Job time : 16.4676 secs

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1921
1 STITHLQQRIVKLQPLSEKE......RSHFHLKAKGVTCYVAGRAF 358
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                                                              May 27, 2003, 15:00:45; Search time 12.9728 Seconds
GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                              283224 seqs, 96134422 residues
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Maximum Match 160%
Listing first 45 summaries
                                         OM protein - protein search, using sw model
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T25390
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T26275
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T32309
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T34405
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Maximum DB seq length: 2000000000
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Match Length DB
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Perfect score:
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Cyacossion: A36647
Cyacossion: A36647
Rilarson, R.D.; Ernst, L.K.; Nair, R.P.; Lowe, J.B.
Proc. Natl. Acad. Sci. U.S.A. 87, 6674-6678, 1990
A;Fitler Molecular cloning, sequence, and expression of a human GDP-L-fucose:beta-D-g
A;Reference number: A36047; MUID:90370848; PMID:2118655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C:Species: Homo sapiens (man)
C:Date: 16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change 10-Sep-1997
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    PVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLH 160
                                               PVLAPEVNRRTSWKQLLLHDWMSEEYSRLEDPFLKFTGFPCSWTFFHHVREQIRREFTLH 188
                                                                                                                          DHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM 218
                                                                                                                                                                                             FRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    268 TQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 GNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMH 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 AALAPVFRITLPVLAPEVDSRTPWRELQLHDWMSEEYADLRDPFLKLSGFPCSWTFFHHL
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                                                                                                                                                                                                                                                                                    galactoside 2-alpha-L-fucosyltransferase (EC 2.4.1.69) - human
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Matches 195; Conserv
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A;Molecule type: mRNA
A;Residues: 1-365 <LAR>
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  101
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              C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 05-Nov-1999
C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 05-Nov-1999
C:Accession: B56392
R:Hitoshi, S.; Kusunoki, S.; Kanazawa, I.; Tsuji, S.
J. Biol. Chem. 270, 8844-8850, 1995
A:Title: Molecular cloning and expression of two types of rabbit beta-galactoside alphal A:Reference number: A56392; MUID:95238380; PMID:7721792
A:Accession: B56392
A:Status: preliminary
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C.Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 05-Nov-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 NINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTL 300
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                                                                                                                                                                                                                                                                                  A;Cross-references: GB:X80225; NID:g854356; PIDN:CAA56512.1; PID:g854357
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C;Keywords: transmembrane protein
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beta-galactoside alphal, 2-fucosyltransferase II - rabbit
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R;Hitshi, S.; Kusunoki, S.; Kanazawa, I.; Tsuji, S.
J. Biol. Chem. 270, 8844-8850, 1995
A;Title: Molecular cloning and expression of two types c
A;Reference number: A56392; MUID:95238380; PMID:7721792
A;Accession: A56392
                                                                                                                                                                                                                                                                                                                                                     67.5%; Score 1296.5; DB 2; 73.9%; Pred. No. 6.8e-101; tive 25; Mismatches 44;
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58.7%; Pred. No. 3.1e-83;
Live 50; Mismatches 59;
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Matches 244; Conservative
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A; Residues: 1-373 <HIT>
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A; Residues: 1-354 <HIT>
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Aganonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A/fittle: Genome Sequence of the nematode C. elegans: a platform for investigating bio A/fittle: Genome Sequence of the nematode C. elegans: a platform for investigating bio A/fittle: Genome Sequence of MUID:99069613; PMID:981916
A.Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_A/Accession: H87911
A.Accession: H87911
A.Accession: H87911
A.Accession: H87911
A.Molecule type: DNA
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-443 <STO>
A.Cross-references: GB:chr_I; PIDN:AAC16988.1); PID:93150470; GSPDB:GN00019; CESP:B020
A.Note: contains weak similarity to fucosyltransferases
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 28-Jul-2000
C;Accession: T44228
C;Accession: T44228
Gene 237, 321-332, 1999
A;Title: The genes responsible for O-antigen synthesis of Vibrio cholerae 0139 are classecence number: 222749; MUID: 99453293; PMID: 10521656
A;Accession: T44228
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Cross-references: EMBL:AB012957; NID: 94115688; PIDN: BAA33632.1; PID: 93721682
A;Experimental source: strain 022
A;Experimental source: st
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: LO-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: H87911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LGNOMGEYATLFALARMNGRLAFIPA -- SMHNA -- LAPIFRISLPVLHSDTAKKI ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.2%; Score 214.5; DB 2; Length 281; larity 26.5%; Pred. No. 2.1e-10; Conservative 50; Mismatches 102; Indels 67.
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Best Local Similarity 20.64
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
hes 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DTAKKIPWQNYHL-
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A;Gene: B0205.4
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Matches
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A; Status: preliminary
A; Molecule type: mRNA
A; Cross-references: EMBE:L26009; NID:9414814; PIDN:AAB41514.1; PID:9554438
B; Piau, J.P.; Labarriere, N.; Dabouis, G.; Denis, M.G.
B; Piau, J.P.; Labarriere, N.; Dabouis, G.; Denis, M.G.
A; Fitle: Evidence for two distinct alpha-(1,2)-fucosyltransferase genes differentially
A; Reference number: S46493; MUID:94280382; PMID:8010942
....... Evidence for two distinct alpha-(1,2)-fucosyltransferase genes differentially A;Reference number: $46493; MUID:94280382; PMID:8010942 A;Accession: $46494 A:Monleyni + 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Rattus norvegicus (Norway rat)
C;Dacate: 07-May-1995 #sequence_revision 17-Nov-1995 #text_change 08-Oct-1999
C;Accession: S51582: S46403
R;Plau, J.P.; Labarriere, N.; Dabouis, G.; Denis, M.G.
submitted to the EMBL Data Library, November 1993
A;Reference number: S51582
A;Reference number: S51582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 PAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIXLANYTLPDSPFLKVFKPBAAFLPEW 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                  200 NVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGS 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 260 PAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEW 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 PCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVN--GSQPSTFVGVHVRRGDYVHV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198 MPNVWKGYVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIE 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 VGIPADLSPILKALTPACPRSHFHLKAKGVTCYVAGRAF 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 VGIPADLSPLLKALTPACPRSHFHLKAKGVTCYVAGRAF 358
                                                                                                                                                                                                                                                                                                                           Score 846; DB 2;
Pred. No. 1.3e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 581; DB 2;
Pred. No. 1.8e-41;
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A,Residues: 9-135 <PI2>
A,Cross-references: EMBL:L26009
C,Keywords: glycosyltransferase
                                                                                                                                                                                                                                   A,Gene: FTB
C;Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Mismatches
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                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.4%;
Matches 158; Conservative
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                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-159 <PIA>
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Db 163 ASKITLTSCCAYRULSTILPNDSRIIERIDGYFONFRYFHPDSQKIVKKLFTFM 216 Qy 161 DHVREEAQAF	hypothetical protein C17A2.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans

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C; Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jul-2000 C; Accession: T31916
R; Sammons, L.; Wohldmann, P.
Submitted to the EMBL Data Library, July 1997
A; Description: The sequence of C. elegans cosmid C17A2.
A; Reference number: Z21098
A; Reference number: Z21098
A; Reterence number: Z31916
A; Accession: T31916
A; Molecule type: DNA
A; Residues: 1348 < SAM>
A; Residues: 1348 < SAM>
A; Residues: 1348 < SAM>
A; Cross-references: EMBL:AF016654; PIDN:AAB66030.1; GSPDB:GN00020; CESP:C17A2.4
A; Experimental source: strain Bristol N2; clone C17A2
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R) Bauer, C.; Clarke, K.
Submitted to the RNBL Data Library, September 1997
A) Description: The sequence of C. elegans cosmid K06H6.
A) Reference number: Z21147
A) Accession: T32294
A) Accession: T32294
A) Status: preliminary; translated from GB/EMBL/DDBJ
A) Residues: 1-335 < DAV>
A) Residues: 1-335 < DAV>
A) Cross-references: EMBL: AF024500; PIDN: AAB70365.1; GSPDB:GN00023; CESP: K06H6.6
A) Experimental source: strain Bristol N2; clone K06H6
C) Genetics:
A) And Construction of Construc
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A;Introns: 17/1; 32/2; 58/1; 111/3; 150/3; 184/2; 218/1; 243/3; 272/1; 303/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C14C6.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein K06H6.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158 TLHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGV-VADRGYLEKAL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 SIGRLGNOMGEYATLFALARMNGR--LAFIPASMHNALAPIFRISLP------VLHSDT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 AKKI---PWQ-----NYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEF 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 DMFRARYSSPV-----FVVTSNGMAWCR---EN--INASRGDVVFAGNGI--EGSPA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 SPSRLGNHIFEFRALLFERSERLHRIPLFLYENEFHQKMLDETRKYMPGLYEKFTVINGSL 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 2
A;Introns: 94/3; 133/3; 168/2; 272/1
C;Superfamily: Caenorhabditis elegans hypothetical protein C14C6.3
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8.0%; Score 153.5; DB 2; Length 335;
Best Local Similarity 22.8%; Pred. No. 3.5e-05;
Matches 77; Conservative 50; Mismatches 118; Indels 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

8.0%; Score 154; DB 2; Length 348
Best Local Similarity 22.8%; Pred. No. 3.3e-05;
Matches 63; Conservative 53; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262 KDFALLTQ-CNHTIMTI--GTFGIWAAYLAGGDTIY 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: CESP:C17A2.4
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Wed May 28 09:23:04 2003

RESULT 13 T22068 hypothetical protein F41D3.6 - Caenorhabditis C.Species: Caenorhabditis elegans C.Date: 15-Oct-1999 #sequence_revision 15-Oct- C.Accession: T22068 R.Winite, S. Submitted to the EMBL Data Library, November 3 A.Reference number: 219508 A.Reference number: 219508 A.Status: preliminary; translated from GB/EMBI A.Molecule type: DNA A.Molecule: 1-500 CWILL> A.Cross-references: EMBL:281537; PIDN:CAB04377 A.Experimental source: clone F41D3 C.Genetios: A.Gene: CESP:F41D3.6 A.Map postilon: 1 A.Throne: 03/1: 54/1 112/2: 150/2: 222/1. 27	Query Match Best Local Similarity 7.2%; Score 138.5 Best Local Similarity 23.4%; Pred. No. 0 Matches 74; Conservative 48; Mismatche QY 52 MFTINSIGRIGNOMGENATIFALARMNGRIAFIPAR Db 49 MTTINYKGGLGNQIEFULSILGIARKIKRIA QY 98ISLPVLHSDTAKKIPWQNYHINDW DD 104 EQUISVPIEPSETIRFAISSDCCRYELSDNHIADD QY 147 HHLRPEILKEFTLHDHYREEAQAFLRGLRVNGSQPR QY 203 KGVVADRGYLEKALDMFRARYSBPVFVYTGNGAWW DD 156 ADWARSTISAIDHLRSLYHGVIFIM-SNDFKWN QY 204 T-AGTDSNYTISAIDHLRSLYHGVIFIM-SNDFKWN QY 263 DFALLTQCNHIIMTGTFR DD 249 DIRIMKTLMEDAIDDLHFSQIYCDSVLITARSSTER QY 304 PFLKVFKPEAAFLDEW 319 Db 249 DIRIMKTLMEDAIDDLHFSQIYCDSVLITARSSTER QY 305 VQLQMTK-EDFYPPTW 323 RESULT 14 H71976 Probable alpha(1,2)fucosyltransferase - Helioc C;Species: Helicobacter Pylori A;Variety: strain 399 C;Date: 12-Feb-1999 f*sequence_revision 12-Feb-	C;Accession: H1976 R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, E 7; Tres. C.; Gibson, R.; Merberg, D.; Mills, S. Nature 397, 176-180, 1999 A;Title: Genomic sequence comparison of two ut A;Reference number: A71800; MUID:99120557; PMA A;Accession: H71976 A;Status: pre-liminary A;Molecule type: DNA A;Residues: 1-299 ARN> A;Cross-references: GB:AE001447; GB:AE001439; A;Cross-references: strain J99 C;Genetics: C;Genetics: A;Gene: jhp0086 C;Superfamily: Vibric cholerae hypothetical pu
OY 87 SMHNALAPIERISLPVLHSDTAKKIPWONYHLNDWMEER 125 :::: :: :: :: :: :: :: :: :: :	PRESCUT 12 120572 PURPORT PURP	QY 179 SQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRAFYSSPVFVVTSN 233

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unrelated isolates of the human gastric p
PMID:9923682
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                                                                                                                                           77.1; GSPDB:GN00019; CESP:F41D3.6
                       t-1999 #text_change 15-Oct-1999
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                                                                                                                                                                                                                                    5; DB 2; Length 500;
0.001;
thes 105; Indels 89; Gaps
                                                                                                                                                                                                                                                                                                             PSTFVGVHVRRGDYV ---- HVMPNVW 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WMEERYRHIPGHFVRFIGYPCSWTFY 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cobacter pylori (strain J99)
                                                                                                                                                                                                             278/1; 308/3; 326/3; 421/3
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A;Introns: 50/1; 80/2; 140/3; 179/3; 218/2; 253/1; 278/1; 306/3; 325/1; 342/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C14C6.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:281132; PIDN:CAB03434.1; GSPDB:GN00023; CESP:T26E4.4
A;Experimental source: clone T26E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apported to protein T26E4.4 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Accession: T2309 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000 R; McMurray, A. Submitted to the EMBL Data Library, October 1996 A; Reference number: Z20013 A; Reference number: Z20013
                                                                                                                                                                                                                                                         70 QHEPKLVRDALKYMGFDRVSQEIVFEYEPKLLKPSRLTYFYGYFQDPRYFDAISSLIKQT 129
                                                                                                                                                                                                               100 --LPVLHSDTAKKIPWQNYHLNDWMEERYRHI-PGHFVRFTGYPCSWTFYHHLRPEILKE 156
                                                                                                                                                                                                                                                                                                                           FTL----HDHVREEAQAFLRGLR-VNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRG 210
                                                                                                                                                                                                                                                                                                                                                               -----LLTQCNHTIMTIGTFGIWAAYLAG--GDTIYLANYTLPDSPFLKVFKPEAAF 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228 EEAYWDMLLMQSCKHGIIANSTYSWWAAYLINNPGKIII------GPKHWLFGHENIL 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GNOMGEYATLFALARMNGRLAFIPA-----SMHNALAPIFRISLPVLHSDTAKKIPWQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 NY--HLNDWME------ERYRHIPGHFVRFIGYPCSWTFYHHLRPEILKEFT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 ATDFLVKHYOKWHYRTTVVVVFGNDVNFSKAVFEDRVSNSSVIPNRTTPPLNFPIPENSPK 304
                                                              Gaps
                                                                                                                                                      GGLGNQMPQYAFAKSLQKHSNTPVLLDITSFDGSNRKMQLELFPIDLPYASAKEIAIAKM 69
                                                                                                         59 GRLGNQMGEYA------TLFALARMNGRLAFIPASMHNALAPIFRIS-- 99
                                                                                                                                                                                                                                                                                                                                                                                                                                      211 YLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 YOKKAVEYMAKRVPNMELFV-----FCE------DLKFTQNLDLGYPFMDMTTRDKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159 LHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDY----VHVMPNVWKGVVADRGYLEK
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6.9%; Score 133.5; DB 2; Length 299; 22.9%; Pred. No. 0.0014; live 38; Mismatches 129; Indels 89
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6.8%; Score 131; DB 2; Length 365;
Best Local Similarity 20.7%; Pred. No. 0.003;
Matches 61; Conservative 43; Mismatches 106; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A;Residues: 1-365 <WIL>
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                      22.98;
  Query Match 6.9
Best Local Similarity 22.9
Matches 76; Conservative
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A:Gene: CESP:T26E4.4
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- protein search, using sw model OM protein

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(without alignments)
1417.108 Million cell updates/sec

US-10-040-863-8_CCPY_23_380

1921 1 STIIHLQQRIVKLQPLSEKE.....RSHFHLKAKGVTCYVAGRAF 358 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 segs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB s Maximum DB s Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	QI.	PIG	FUT2_BOVIN	FUT2_HUMAN	FUT2_MOUSE	FUT2_RABIT	FUT1_MOUSE	FUT1_RAT	FUT1_RABIT	FUT1_HUMAN	FUT1_PIG	FUT2_RAT	YKQ7_CAEEL	VGLD_HSVEK	FMA3_PORGI	CDH_PHACH	MY10_HUMAN	PTN7_RAT	VGLD_HSVEA	VGLD_HSVEB	GRB2_MOUSE	GRB2_HUMAN	NQO1_THETH	QUTD_EMENI	CN3B_HUMAN	PLO3_HUMAN	LPH_RAT	RIBB_HELPY	AAT_THEAQ	CTPC_MYCTU	POLG_MVEV	TC1A_CAEEL	FMB2_PORGI	CYB_PARDE
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Q61409 mus musculu	P76464 escherichia			P87503 hūman adeno	P97846 rattus norv	P78357 homo sapien	P87379 xenopus lae	Q9z140 helicobacte	P23739 rattus norv		054991 mus musculu
CN3B_MOUSE	YFAS_ECOLI	GSPN_VIBCH	GLO2_SYNY3	DPOL_ADE04	CTA1_RAT	CTA1_HUMAN	GRB2_XENLA	RIBB_HELPJ	SUIS_RAT	Y285_MYCGE	CTA1_MOUSE
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83.5	83.5	8 8	82.5	82.5	82.5	82.5	82	82	82	81.5	81.5
34	35	36	37	38	39	40	4 1	42	43	44	45

ALIGNMENTS

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               010982; Q29044; O19100; O1-027-1996 (Rel. 34, Created)
01-027-1996 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
63-Jetcoside 2-1-fucosyltransferase 2 (EC 2.4.1.69) (GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase 2) (Alpha(1,2)FT 2)
                                                                                                                                                                                                                                                                                                                      MEDIINE-97468270; PubMed=9321466; Masabanda J., Wigger G., Meifarink E., Fries R., Voegall P., Masabanda J., Wigger G., Stricker C., Neubnschwander S., Bertschinger H.U., Stranzinger G.; Two alpha(1,2) fucosyltransferase genes on porcine chromosome 6q11 are closely linked to the blood group inhibitor (S) and Escherichia are clisely linked (ECP187) loci."; Mann. Genome 8:736-741(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
-!- PATHAAY: Glycosylation.
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISIERNAE OF GOLGI (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thurin J., Blaszczyk-Thurin M.;
"Porcine submaxillary gland GDP-L-fucose: beta-D-galactoside
alpha-2.-L-fucosyltransferase is likely a counterpart of the human
Secretor gene-encoded blood group transferase.";
J. Biol. Chem. 270:26577-26580(1995).
-!- CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP +
                                                                                                                                                                                                                  Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. Cohney S., McKenzie I.F.C., Sandrin M.S.; Cohney S., Mouhtouris E., McKenzie I.F.C., Sandrin M.S.; "Molecular cloning and characterization of the pig secretor type alpha(1,2)fucosyltransferase."; Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                            Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,
340 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECTENCE OF 69-80; 119-133 AND 316-334.
TISSUE-Submaxillary gland;
MEDLINE-96064742; PubMed=7592879;
PRT;
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SIANDARD;
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FUT2_PIG
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30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 2 (EC 2.4.1.69) (GDP-L-fucose:Deta-D-galactoside 2-alpha-L-fucosyltransferase 2) (Alpha(1,2)FT 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
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                                                                                                                           SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
                                                                                                                                                                                                                                                                                                         Gaps
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-!- CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP +
alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
-!- PATHRAX: Glycosylation.
-!- PATHRAX: Glycosylation.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                   STITHLQORIVKLOPLSEKELPMITQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR
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                                                                                                                                                        LUMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
R -> H (IN REF. 3).
                                                                                                                                                                                                                                                                                                        14;
         EMBL; U70881; AAB81883.1; -.
EMBL. AF027304; AAC9170.1; -.
EMBL. X98621; CAAC9170.1; -.
InterPro; IPR002516; GI_11.
Pfan; PF01531; Glyco_transf_11; 1.
Transferase; Glycoxyltransferase; Glycoprotein; Transmembrane; Golg: stack; Signal-anchor.
                                                                                                                                                                                                                                                                        tch 75.5%; Score 1451; DB 1; Length 340; al Similarity 81.9%; Pred. No. 1.9e-115; 271; Conservative 26; Mismatches 20; Indels 14
                                                                                                                                                                                                                                               0629F1C04FC206AD CRC64;
                                                                                                               CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   344 AA
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340 AA;
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Q28113;
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CARBOHYD
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 2 (EC 2.4.1.69) (GDP-L-fucose:beta-
D-galactoside 2-alpha-L-fucosyltransferase 2) (Alpha(1,2)FT 2)
(Fucosyltransferase 2) (Secretor blood group alpha-2-
fucosyltransferase) (Secretor factor) (Se) (SE2).
                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL). SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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                                                                                                                                                                                                                                                          (POTENTIAL).
LUMENAL, CATALIIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
W. F35AC33F1B7B9F68 CRC64;
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Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                          InterPro; IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                             73.6%; Score 1414; DB 1; Length 344; 78.9%; Pred. No. 2.5e-112; ive 25; Mismatches 35; Indels 10
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MEDLINE-95181460; PubMed-7876235;
Kelly R.J., Rouquier S., Giorgi D., Lennon G.G., Lowe J.B.;
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Mammalia; Eutheria; Primates;
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                                                                                                                                              EMBL; X99620; CAA67931.1; -.
                                                                                                                                                                                                               Golgi stack; Signal-anchor.
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51; Conservative
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CARBOHYD
CARBOHYD
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SEQUENCE
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Best Local
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SIGNAL-ANCHOR (TYPE-11 MEMBRANE PROTEIN).
LUMENAL, CATALYTIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (1,2)GALBETA-) CALLED THE HANTIGEN WHICH IS AN ESSENTIAL SUBSTRATE FOR THE FIRAL STEP IN THE SOLUBLE A AND B ANTIGEN SUBSTRATE FOR THE FIRAL STEP IN THE SOLUBLE A AND B ANTIGEN SYNTHESIS PATHWAY. H AND SE BUZYMES FUCOSYLATE THE SAME ACCEPTOR SUBSTRATES BUT EXHIBIT DIFFERENT KM VALUES.

-!- CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP + alpha-L-fucosyl-1,2-beta-D-galactosyl-R.

-!- PATHWAY: Glycosylation.

-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
    blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FORM IN TRANS CISTERNIA OF GOLGI.

-1-ALTERNATIVE PRODUCTS: TWO FORMS ARE PRODUCED BY THE USE OF
ALTERNATIVE PRODUCTS: TWO FORMS ARE PRODUCED BY THE USE OF
ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.
-1-TISSUE SPECIFICITY: SMALL INTESTINE, CCLON AND LUNG.
-1-MISCELLANBOUS: THERE ARE TWO GENES (FUTI AND FUT2) WHICH ENCODE
GALACTOSIDE 2-L-FOCOSYLIRANSFERSSION RESTRICTED TO CELLS OF
MESODERNAL OR ENDODERNAL ORIGIN RESPECTIVELY.
-1-SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                           (2)
SEQUENCE FROM N.A., AND VARIANT PHE-140.
MEDLINE=96199252; PubMed=8621666;
Kudo T., Iwasaki H., Nishibara S., Shinya N., Ando T., Narimatsu I.,
"Sequence and expression of a candidate for the human Secretor blood group alpha(1,2)fucosyltransferase gene (FUT2). Homozygosity for an enzyme-inactivating nonsense mutation commonly correlates with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    !- FUNCTION: CREATES A SOLUBLE PRECURSOR OLIGOSACCHARIDE FUC-ALPHA
                                                                                                                                                                        system. II. Secretor gene inactivation by a novel single missense mutation A385T in Japanese honsecretor individuals."; J. Biol. Chem. 271:9830-9837(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T., du Toit E.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LONG ISOFORM.
GALACTOSIDE 2-L-FUCOSYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GALACTOSIDE 2-L-FUCOSYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Extensive polymorphism of the FUT2 gene in an African (Xhosa) population of South Africa."; Hum. Genet. 103:204-210(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfan, PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
Signal-anchor; Golgi stack; Alternative initiation;
                                                                                                                                                                                                                                                                                                                              Koda Y., Soejima M., Wang B., Kimura H.;
"Structure and expression of the gene encoding secretor-type
galactoside 2-alpha-L-fucosyltransferase (FUT2).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Koda Y., Soejima M., Pang H., Schlaphoff
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                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND VARIANT PHE-140,
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VARIANTS VAL-25; CYS-138 AND ASN-172.
MEDLINE=98431007; PubMed=9760207; CAA-178 M.P. Pang H.,
                                                                                                                                                                                                                                                                                                                                                                                         Eur. J. Biochem. 246:750-755(1997).
                                                          non-secretor phenotype.";
J. Biol. Chem. 270:4640-4649(1995).
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                                                                                                                                                                                                                                                                                                                  MEDLINE=97363210; PubMed=9219535;
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243
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15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu Y., Ko
Kimura H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INIT_MET
DOMAIN
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
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"Molecular cloning and expression of a GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase in murine gastrointestinal tract."; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 2 (EC 2.4.1.69) (GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase 2) (Alpha(1,2)FT 2)
FUT2 OR SEC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 WMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 PSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRE 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 STIIHHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hitoshi S., Kusunoki S., Kanazawa I., Tsuji S.; "Molecular cloning and expression of a mouse GDP-L-Fucose: beta-D-alactoside 2-alpha-L-Fucosyltransferase."; Submitted (DEC-1996) to the EMEL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 STIFHVQQRLAKIQAM--WELPV-----QIPVLASTSKALGPSQLRGWWTINAIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I -> F (IN JAPANESE SEJ ALLELE; NON-
(GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                                       73.3%; Score 1407.5; DB 1; Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lin B., Hayashi Y., Saito M., Sakakihara Y., Yanaqisawa M.,
Iwamori M.;
                                                                                                                                                                                                                                                          /FTId=VAR_003424
D -> N (IN XHOSA POPULATION).
/FTId=VAR_003425.
                                                                                                                                             R -> C (IN XHOSA POPULATION).
/FTId=VAR_003423.
                                                                                       I -> V (IN XHOSA POPUĽAŤION).
/FTId=VAR_003422.
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                                                                                                                                                                                                                                                                                                                                                                  12066D9CF175E13A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       . No. 9e-112;
. No. 9e-112;
. hes 32;
                                                                 GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       368 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=ICR; TISSUE=Gastrointestinal tract;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   312 PDSPFLKIFKPEAAFLPEWTGIAADLSPLLK 342
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                            N-LINKED (
N-LINKED (
I -> V (IN
                                                                                                                                                                                                                                           SECRETOR
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                                                                                                                                                                                                                                                                                                                                                                  39017 MW;
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                                                                                                                                                   138
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                                                                                                                                                                                                                                                                                                                                                              343 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                      138
                                                                                                                                                                                                           140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUT2_MOUSE
P97353;
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
      CARBOHYD
                                  CARBOHYD
                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 PSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 NINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STASRGDVAFAGNGLGGSPAKDIALLMQCNHTVITLGTFGINAAYLTGGDTVYLANFTQ 318
                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
                                                                                                                                                                                                                                                                                                                                                                                                                                36; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-TUN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-tucosyltransferase 2 (EC 24.1.69) (Secretor blood group alpha-2-fucosyltransferase) (GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase 2) (Alpha(1,2)FT 2) (Fucosyltransferase 2).
                       PATHWAY: Glyoosylation.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
FORM IN TRANS CISTERNAE OF GOLGI (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STITHLQORIVKLOPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STIFHCHRRL-----GRVPAPWASPSLVVFPPRHMPRE--GMFTIRVKGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 WMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQ
                                                                                                                                                                                                                                                                                                                               LUMENAL, CATALFIC (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
                                                                                                                                                                                                                                          Interpro; IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 368;
                                       MISCELLANBOUS: THERE ARE TWO GENES (FUT1 AND SEC1) WHICH SIMILARITY).
SIMILARITY SEC1.FUCOSYLITANSFERASE.
CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
                                                                                  SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11
                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. .) (PC 4093E853EB37303B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        Score 1338.5; DB 1
Pred. No. 6.7e-106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             354 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                21; Mismatches
                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDSPFLKVFKPEAAFLPEWVGIPADL 326
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                                                                                                                                                                                                                                                                                                                               368
195
289
315
41464 MW;
                                                                                                                                                                                                                                                                                                                                                                                                      cch 69.7%;
al Similarity 77.3%;
252; Conservative 21
                                                                                                                                                                                                                     EMBL; AF113532; AAD25351.1;
MGD; MGI:109374; Fut2.
                                                                                                                                                                                                                                                                                 Golgi stack.
                                                                                                                                                                                                        EMBL; Y09882; CAA71008.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                42
195
289
315
368 AA;
                                                                                                                                                                                                                                                                                 Signal-anchor;
DOMAIN
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Q10983;
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S:
Matches 252
                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                             CARBOHYD
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FUT2_RABIT
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                                                                                                                                                                                           TISSUB-BETAIN;

X MEDLINE-95238380; PubMed-7721792;

X MEDLINE-95238380; PubMed-7721792;

A Hitoshi S., Kusunoki S.;

Hitoshi S., Kusunoki S.;

Rollar cloning and expression of two types of rabbit beta-
galactoside alpha 1,2-fucosyltransferase.";

Lu Galactoside alpha 1,2-fucosyltransferase.";

Lu Galactoside alpha 1,2-fucosyltransferase.";

Lu Galactoside alpha 1,2-fucosyltransferase.";

Lu Galactoside alpha 1,2-fucosyltransferase.";

CI,2)GALBETA-) CALLED THE H ANTIGEN WHICH IS AN ESSENTIAL

SUBSTRATE FOR THE FINAL STPE IN THE SOLUBLE A AND B ANTIGEN

SUBSTRATES BOT EXHIBIT DIFFERENT KM VALUES.

COTALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP +

COTALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP +

ALPHANY: Glycosyl-ation.

COTALICAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND

FORM IN TRANS CIGERERAR OF GOLGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 NINASRGDVVFAGNGIBGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WHICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 SIVFHCHQRLAL------VPAPWAYSARVVVVP------GHLPREGMWTINAMGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 PSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRE
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-!- MISCELLANEOUS: THERE ARE THREE GENES (FUT1, FUT2 AND FUT3) WHI
ENCODE GALACTOSIDE 2-L-FUCOSYLTRANSFERASE IN RABBIT: THEY ARE
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi:
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (LOMENAL, CATALYTIC (POTENTIAL).

N-LINKED (GLCNAC, ) (POTENTIAL).

N-LINKED (GLCNAC, .) (POTENTIAL).

1E2B831F9DA6CCB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X80225; CAA56512.1; -.
InterPro; IPR002516; GT_l1; -.
Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXPRESSED IN A TISSUE-SPECIFIC MANNER.
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.5%; Score 1296.5; DB 1 73.9%; Pred. No. 2.3e-102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40035 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Golgi stack.
1 22
3 43
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197
291
317
354 AA;
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                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                      NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal-anchor;
DOMAIN
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FUT1_RAT
Q10980;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Elechem. J. 327:105-115(1997).

2. I CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP + alpha-L-fucosyl-1,2-beta-D-galactosyl-R.

2. I CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP + alpha-L-fucosyl-1,2-beta-D-galactosyl-R.

2. I CATHWAY: Glycosylation.

2. I SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND CONTRIBUTION TRANS CISTERANE OF GOLGI.

2. I TISSUE SPECIFICITY: IN THE ADULT, HIGHLY EXPRESSED IN PANCREAS, TESTIS AND EPIDIDYMIS AND TO A LESSER SYMENT IN THYMUS, LUNG, STONACH, SMALL INTESTINE, COLON, SPLEEN AND UTERUS. NOT EXPRESSED IN BRAIN, HEART, SKELETAL MUSCLE, KIDNEY, LIVER AND BONE MARROW.

2. MISCELLANGOUS: THERE ARE TWO GENES (FUTI AND FUT2) WHICH ENCODE GALACTOSIDE 2-L-FUCOSYLTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                         (GDP-L-fucose:beta-
261 NIDASRGDVVFAGNGLEGSPAKDFALLTQCNHTVMT.GFFGFWAAYLTGGDTVYLANYTA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
LUMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-NIH Swiss,
BEDINB-9745449;
Domino S.E. Hiraiwa N., Lowe UB.;
Molecular cloning, Chromosomal assignment and tissue-specific
expression of a murine alpha(1,2)fucosyltransferase expressed in
thinic and epidioymal epithelial cells.";
                                                                                                                                                                                              15-DEC-1998 (Rel. 37, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L'fucosyltransferase 1 (EC 2.4.1.69) (GDP-L-fucos
D-galactoside 2-alpha-L-fucosyltransferase 1) (Alpha(1,2)FI 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal-anchor; Golgi stack,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.5%; Score 1105.5; DB 1; Lung. 8%; Pred. No. 3.6e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21F1D24CFE2C4106 CRC64;
                                                                                                                                                       376 AA.
                                301 PDSPFLKVFKPEAAFLPEWVGIPADLSPLL 330
                                                   321 PDSPFHLVFKPEAAFLPEWVGITANMGRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01531; Glyco_transf_11; 1.
                                                                                                                                                                                    (Rel. 37, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42255 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U90553; AAC53492.1; -.
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modified and this statement
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                                                                                                                                                     STANDARD:
                                                                                                                                                                                                                                                                     (Fucosyltransferase 1).
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376
67
302
328
                                                                                                                                                                                                                                                                                                   musculus (Mouse)
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328
376 AA;
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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                                                                                                                                                                                15-DEC-1998 (
15-DEC-1998 (
15-JUN-2002 (
                                                                                                                                                FUT1 MOUSE 009160;
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Best Local Simi
Matches 208;
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SEQUENCE
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15 PLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEXATLFAL 74

Conservative

Similarity

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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 1 (BC 2.4.1.69) (GDP-L-fucose:beta-begalactoside 2-alpha-L-fucosyltransferase 1) (Alpha(1,2)FT 1)
75 ARMNGRLAFIPASMHNALAPIFRISLPVLESDTAKKIPWQNYHLNDWMEBRYRHIPGHFV 134
                                           RFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPS-TFVGVHVRRGD 193
                                                                                                                                                                                                                                                          253
                                                                                                                                                                                                                                                                                                                     284
                                                                                                                                                                                                                                                                                                                                                                                 313
                                                                                                                                                      194 YVHVMPNVWKGVVADRGYLEKALDMFRARYSŞPVFVVTSNGMAWCRENINASRGDVVFAG
                                                                                                                                                                                                                                                                             NGIEGSPAKDFALLTQCNFTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEA
                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Two distinct rat GDP-L-fucose:b-D-galactoside 2-alpha-L-fucosyltransferase genes.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          376 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  314 AFLPEWVGIPADLSPLLKALTPACPRSHFHL 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       345 AFLPEWVGINADLSPLQAOFDPWKPDSLFRL 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Soejima M., Wang B., Koda Y., Kimura H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94280382; PubMed=8010942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB015637; BAA31130.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 169-310 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Fucosyltransferase 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IISSUE=Colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
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01-0c1-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 1 (EC 2.4.1.69) (GDP-L-fucose:beta-
D-galactoside 2-alpha-L-fucosyltransferase 1) (Alpha(1,2)FT 1)
                                                                                                                                                                                                                                                                                                              75 ARMNGRLAFIPASMENALAPIFRISLPVLESDTAKKIPWQNYHLNDWMEERYRHIPGHFV 134
                                                                                                                                                                                                                                                                                                                                                                      135 RFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVN--GSQPSTFVGVHVRRG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 GNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPE 312
                                                                                      SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                  53 PVAMVCLPYPSNASSGSPSCPE-----OSLLSGTWTITPGGRFGNQMGQYATLLAL 103
                                                                                                                                                                                                                                                                                                                                  252
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                                                                                                                                                                                                                                                         PLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFAL
                                                                                                                                                                                                                                                                                                                                                                                                                              DYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- PATHWAY: Glycosylation.
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.
-!- TISSUE SPECIFICITY: BRAIN.
                                                                                                            LUMENAL, CATALYTIC (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

C350C737C758B7F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                  11;
EMBL; L26009; AAB41514.1; -.
InterPro; IPR002516; Gr_11.
Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal-anchor; Golgi stack.

CYTOPLASMIC (POFFNTIAL)

1 12 CYTOPLASMIC (POFFNTIAL)
                                                                                                                                                                                                      DB 1; Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hitoshi S., Kusunoki S., Kanazawa I., Tsuji S.,
"Molecular cloning and expression of two types of rabbit beta-
galactoside alpha 1,2-fucosyltransferase.";
J. Biol. Chem. 270:8844-8850(1995).
-!- CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = G
alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
                                                                                                                                                                                                                                  Indels
                                                                         CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                    Score 1101.5; DB Pred. No. 7.8e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  373 AA
                                                                                                                                                                                                                              37; Mismatches
                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAFLPEWVGIPADLSPLLKALTPACPRSHFHL 344
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                                                                                                                                                                        42416 MW:
                                                                                                                                                                                                 57.3%;
ilarity 62.3%;
Conservative 37
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                                                                                                              376
64
302
328
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29
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                                                                                                              30
64
302
328
376 AA;
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207; Conserv
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Q10979;
                                                                                                                           CARBOHYD
CARBOHYD
                                                                                     TRANSMEM
                                                                                                                                                        CARBOHYD
                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                   Match
                                                                                                               DOMAIN
                                                                                                                                                                                                                              Matches
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FUT1_RABIT
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 1 (BC 2.4.1.59) (GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase 1) (Alpha(1.2)FT 1)
(Fucosyltransferase 1) (Blood group H alpha 2-fucosyltransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 SEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISL 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----GIWTIHPDGRFGNOMGOYATLLALAQLNGRRAFILPAMHAALAPVFRITL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM. 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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N-LINKED (GICNAC. .) (POTENTIAL).

N-LINKED (GICNAC. .) (POTENTIAL).

N-LINKED (GICNAC. .) (POTENTIAL).

OA47A1786231525C CRC64;
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominigae; Homo.
GALACTOSIDE 2-L-FUCOSYLTRANSFERASE. THEY ARE EXPRESSED IN A TISSUE-SPECIFIC MANNER WITH EXPRESSION RESTRICTED TO CELLS MESODERMAL OR ENDODERMAL ORIGIN RESPECTIVELY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36;
                                                                                                                                                                                                                                                                                                                                                                                         Interpro: IPR002516; GT_11.
Pfam: PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                       SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 373;
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DOMAIN
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TRANSMEM 13 29
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66
301
327
373 AA;
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Matches 206;
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CARBOHYD
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FUT1_HUMAN
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R InterPro; IPR002516; GT_11.

R Pfam; PF01531; Glyco_transf_11; 1.

Pfam; PF01531; Glyco_transf_11; 1.

R Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;

KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;

FT GNAIN 1 8 25 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).

FT TRANSMEM 9 25 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).

FT CARBOHYD 65 65 N-LINKED (GLCNAC. . ) (POTENTIAL).

FT CARBOHYD 327 327 N-LINKED (GLCNAC. . ) (POTENTIAL).

FT VARIANT 154 154 Y -> C (IN BOMBAY H-).

FT VARIANT 154 154 Y -> C (IN BOMBAY H-).

ATTICHOR (ATTICHOR (TYPE-II MEMBRANE)).

ATTICHOR (TYPE-II MEMBRANE).

ATTICHOR (TYPE-II MEMBRANE).

ATTICHOR (TYPE-II MEMBRANE).

ATTICHOR (TYPE-II MEMBRANE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PATHWAY: Glycosylation.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
FORM IN TRANS CISTERNAE OF GOLGI.
POLYMORPHISM: NONFUNCTIONAL MUTANT OF FUTI ARE THE CAUSE OF THE H-
BOMBAY BLOOD GROUP.
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97445117; Pubmed-9299444; Smart E., Kimura H.; Koda Y., Soejima M., Johnson P.H., Smart E., Kimura H.; Koda Y., Soejima M., Johnson P.H., Smart E., Kimura H.; Missense mutation of Furl and deletion of Furz are responsible for Indian Bombay phenotype at ABO blood group system.; Furcise E. Commun. 238:21-25(1997).

-! FUNCTION: CREATES A SOLUBLE PRECURSOR OLIGOSACCHARIDE FUC-ALPHA SUBSTRATE FOR THE FINAL STEP IN THE SOLUBLE A AND B ANNIGAL SUBSTRATE FOR THE FINAL STEP IN THE SOLUBLE A AND B ANNIGAL SUBSTRATES BUT EXHIBIT DIFFERENT KM VALUES.
-! CAPALYIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP + Albhar-Loosyl-R.
             Larsen R.D., Frist L.K., Nair R.P., Lowe J.B.;
"Modecular cloning, sequence, and expression of a human GDP-L-
"Modes:beta-D-galactoside 2-alpha-L-fucosyltransferase cDNA that can
form the H blood group antigen.";
Proc. Natl. Acad. Sci. U.S.A. 87:5674-6678(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISCELLANDONS: THERE ARE TWO GENES (FUT1 AND FUT2) WHICH ENCODE GALACTOSIDE 2-L-FUCOSYLITRANSFERASE. THEY ARE EXPRESSED IN A TISSUE-SPECIFIC MANNER WITH EXPRESSION RESTRICTED TO CELLS OF MESODERMAL OR ENCODERMAL ORIGIN RESPECTIVELY.

SIMILARITY: BELONGS TO THE GLYCOSYLITRANSFERASE FAMILY 11.
                                                                                                                                                                                                                           VARIANT HIS-164.
MEDLINE-94286534; PubMed=7912436;
Kelly_R.J., Ernst L.K., Larsen R.D., Bryant J.G., Robinson J.S.,
                                                                                                                                                                                                                                                                                        "Molecular basis for H blood group deficiency in Bombay (Oh) and
                                                                                                                                                              "Polymorphism of the h allele and the population frequency of sporadic nonfunctional alleles."; Transfusion 37:284-290(1997).
                                                                                                                                                                                                                                                                                                       para-Bombay individuals.";
Proc. Natl. Acad. Sci. U.S.A. 91:5843-5847(1994).
                                                                                                            SEQUENCE FROM N.A., AND VARIANT ALLELES.
MEDLINE=97240210; Pubmed=9122901;
MEDLINE=90370848; PubMed=2118655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M35531; AAA52639.1; -. EMBL; Z69587; CAA93435.1; -.
                                                                                                                                             Wagner F.F., Flegel W.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC:4012; FUT1.
MIM; 211100; -
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                                                                                                                                                                                                                                                                                                                                                        VARIANT ARG-242
                                                                                                                                                                                                                                                                               Lowe J.B.;
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FUT1_PIG STANDARD: PRT; 365 AA. 029043; O19101; O1.NOV-1997 (Rel. 35. Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 6alactoside 2-L-fucosyltransferase 1 (EC 2.4.1.69) (GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase 1) (Alpha(1,2)FT 1)
                                                                                                                                                                                                                                                                                                                                                                                       90 NALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALL 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         268 TQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                         30 GNTESPEMRKDSEQHGNGELRGMFTINSIGRLGNQMGEXATLFALARMNGRLAFIPASMH 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND VARIANTS THR-103 AND GLN-286.
MEDLINE=97468270; PubMed=9321466;
Meijerink E., Fries R., Voegeli P., Masabanda J., Wigger G., Straicker C., Neuenschwander S., Bertschinger H.U., Straizinger G., Tro alpha(1,2) fuccsyltransferase genes on porcine chromosome 6q11 are closely linked to the blood group inhibitor (S) and Escherichia Mamm. Genome 8:736-741(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 AALAPVERITLPVLAPEVDSRTPWRELQLHDWMSEEYADIRDPFLKLSGFPCSWTFFHHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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                                                                                                                                                                                                                                                                  54.7%; Score 1051.5; DB 1; Length 365; 63.3%; Pred. No. 1.3e-81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cohney S., Mouhtouris E., McKenzie I.F., Sandrin M.S.; "Molecular cloning of the gene coding for pig alphal-->2
                                                                                                                                                                                            /FTId=VAR_003421.
4F4442EC375C9D9E CRC64;
/FTIG=VAR_003418.
L -> R (IN BOWBAY H-).
/FTIG=VAR_009709.
V -> E (IN BOWBAY H-).
/FTIG=VAR_004419.
A -> V (IN BOWBAY H-).
/FTIG=VAR_003420.
M -> C (IN BOWBAY H-).
                                                                                                                                                                                                                                                                                                                 37; Mismatches
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                                                                        259
                                                                                                                       315
                                                                                                                                                                                                                365 AA;
                                                                                                                                                                                                                                                                                 Local Similarity
hes 195; Conserv
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SEQUENCE FROM N.A.
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                        242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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CYTOPLASMIC (POTENTIAL).

SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).

SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).

LUMBENAL, CATALTTIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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Bertschinger H.U., Stranzinger G., Voegeli P.;
Expression and activity of porcine alpha(1.2) fucosyltransferases
determine erythrocyte antigen precursor O status and susceptibility
Escherichia coli F18 colonization in the small intestine.;
Submitted (MAR-1999) to the EMBL/GenBank/DBH databases.
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                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP + alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
-!- PATHWAY: Glycosylation.
-!- PATHWAY: Glycosylation.
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAR OF GOLGI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF136896; AAF59833.1; --
InterPro; IPR002516; GT_11.
Pfam; PF01331; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
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R -> 0.
R -> 0.
L -> F (IN REF. 1).
MW, DAFCE77E89A29D75 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BIOCHEM. J. 300:623-626 (1994).

CHOCATION: CREATES A MEMBRANE-ASSOCIATED PRECURSOR OLIGOSACCHARIDE CONTROL OF THE STATE OF THE TIME STATE WHICH IS AN ENGRENALE FINAL STEP IN THE MEMBRANE-ASSOCIATED CALAND AND SERVITAL SUBSTRATE FOR THE FINAL STEP IN THE MEMBRANE-ASSOCIATED CALAND ESSENTIAL SUBSTRATE FOR THE FINAL STEP IN THE MEMBRANE-ASSOCIATED CALAND SE MAY BE STOCKYLAIF CALAND SE MAY BE STATEMENT KN VALUES:

CALALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP + alpha-L-fucosyl-1, 2-beta-D-galactosyl-R.

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                      01-0CT-1996 (Rel. 34, Lost sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
6alactoside 2-L-fucosyltransferase 2 (EC 2.4.1.69) (Secretor blood group alpha-2-fucosyltransferase) (GDP-L-fucoseheta-D-galactoside 2-alpha-L-fucosyltransferase)
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14DECEB7C2E6384A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Piau J.-P., Labarriere N., Dabouis G., Denis M.G.; "Evidence for two distinct alpha(1,2)-fucosyltransferase genes differentially expressed throughout the rat colon."; Biochem. J. 300:623-626(1994).
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Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
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Score 846; DB 1; Lengu...
-A No. 1.1e-64; Indels
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0; Mismatches
        159
                                                                                                                                                                                                                                                                                                                                           (Fucosyltransferase 2) (Fragment).
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159 AA; 17250 MW;
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STANDARD:
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SEQUENCE FROM N.A.
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Matches 158; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
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FUT2_RAI
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RESULT 12

RESULT 11

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STANDARD;
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Watches 54; Conservative
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422
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423
103
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347
396
442 AA;
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SIGNAL
                                                                                                                                                                                                                                    01-AUG-1991
01-AUG-1991
                                                                                                                                                                                             VGLD_HSVEK
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CARBOHYD
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                                                                                                                                               RESULT 13
VGLD_HSVEK
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                                         01-FEB-1994 (Rel. 28, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative glycosyl transferase C06EL.7 in chromosome III (EC 2.-.-.).
                                                                                                                                                                                                                                                                                                                                                                 Cooper J., Coulson A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 SIGRLGNQMGEYATLFALARMNGR--LAFIPASMHNALAPIFRISLPVLHSD------ 106
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                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    158 ILHDHVREEAQAFLRGL----RVNGSQPSTFVG---VHVRRGDYV---HVMPNVWKGVVA 207
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                                                                                                                                                                                                                                                                                                                            Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Sims M., Smaldon N., Smith A., Saunders D., Shownkeen Sims M., Smaldon N., Smith M., Sonhhammer B., Staden R.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
Wohldman P.,
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---DKYKEKVQSFVKPAIDFSPLPNSDSSNFISRICIHIRRTDFVDGQHHSSNV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
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Pfam; PF01531; Glyco, transf_l1; 1.
Hypothetical protein; Transferase; Glycosyltransferase.
SEQUENCE 365 AA: 41991 MW; B5FPCA363F31977F CRC64:
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                                                                                                                                                                                                  Rhabditidae, Peloderinae; Caenornabditis
NCBI_TaxID=6239;
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MEDLINE=94150718; PubMed=7906398;
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WormPep; C06E1.7; CE30483.
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    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 368:32-38(1994).
                                                                                                                                                      Caenorhabditis elegans,
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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CAEEL
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REVISIONS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIANE=91082407; PubMed=1845821; Flowers C.C., Eastman E.M., O'Callaghan D.J.; "Sequence analysis of a glycoprotein D gene homolog within the unique short segment of the EHV-1 genome."; Virology 180:175-184(1591).
278 KYFVS---ENTPQDDLAYSHYSCDATLITAPSSTFGWWLGYLSKGQAVYYQDIRSTNDVN 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 234 LYRRVIEIDGRRIYTDFSVTIPSERCPIAFELNEGN---PDRCKMPEGYSRGE---VFTR 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92263758; pubMed=1316673; Colle C.F. III, Flowers C.C., O'Callaghan D.J.; Open reading frames encoding a protein. Winase, homolog of 91ycoprotein gX of pseudorabies virus, and a novel glycoprotein map within the unique short segment of equine herpesvirus type 1."; Virology 188:545-557(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY.
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N-LINKED (GECNAC. .) (POTENTIAL).
N-LINKED (GECNAC. .) (POTENTIAL).
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31; Mismatches 103; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Equine herpesvirus type 1 (strain Kentucky A) (EHV-1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
NCBI_TaxID=10329;
                                                                                                                                                                                                                                                                                                                                                                                            update)
on update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein D precursor (Glycoprotein 17/18)
GD OR GP17/18 OR 72.
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                                                                                                                                                                                                                                                                                                                                                 01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
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EMBL, M87497, AAA46073.1; ALT_INIT.
PINS, NGBEBA.
INTERPRES IPRO02896; Herpes_glycop_I
Pfam; PF01537; Herpes_glycop_D; 1.
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                                                              305 FLK-VFKPEAAFLPEWVGIPAD 325
                                                                                                                          335 YKKGVLDPDDFFVPSWTSIMLD 356
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                                   114 ONYHLNDWMEERYRH----IPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQ 168
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                                                                     332 DNHPGFDSVESEITQNKTDPKPGQADPKPNQPFKWPSIKHLVPRL------DEVDEVIE 384
           --FARPVPP 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fujiwara T., Morishima S., Takahashi I., Hamada S., "Molecular cloning and sequencing of the fimbrilin gene of Porphyromonas gingivalis strains and characterization of recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT PROTEIN, TYPE III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Finbrillin is the structural subunit of the fimbriae, that are filamentous appendages on the cell surface. Fimbriae of P.gingivalis are recognized as a major virulence factor as they mediate cell adhesion and play an important role in invasion of
                                                                                                         169 AFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSP 226
                                                                                                                                 385 PVIKPPKISKSN-STFVGISVGLGIAGLVLVVGVILYVCLRR---KKELKVCTERLDSP 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Functional differences among FimA variants of Porphyromonas gingivalis and their effects on adhesion to and invasion of human epithelial cells.":
Infect. Immun. 70:277-285(2002).
                                                                                                                                                                                                                                                                  15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Major fimbrial subunit protein, type III precursor (Fimbrillin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Fimbria.
SIMILARITY: BELONGS TO THE P.GINGIVALIS FIMBRILLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21614934; PubMed=11748193;
Nakagawa I., Amano A., Kuboniwa M., Nakamura I., Kawabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 89; DB 1; Length 353;
; Pred. No. 3.3;
38; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAJOR FIMBRIAL SUBUNIT PR.
7FBE4FBF427EA2AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                             Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides; Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. Biophys. Res. Commun. 197:241-247(1993).
288 RFLGEFNFPQGEHMTWVKFWFVYDGGNL---PVQFYEAQA--
                                                                                                                                                                                                                                            353 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION, AND CLASSIFICATION INTO TYPES.
                                                                                                                                                                                                                                                                                                                                                                                                                   Porphyromonadaceae; Porphyromonas.
NCBI_TaxID=837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94071950; PubMed=7902712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          353. N
38024 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D17801; BAA04627.1;
                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10
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353 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     periodontal
                                                                                                                                                                                                                                                                                                                                          (Fimbrilin).
                                                                                                                                                                                                                                   FMA3_PORGI
Q51826;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=6/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hamada S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteins.
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                                                                                                                                                                                                                  FMA3_PORGI
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                     191 ITFNGAYSPANYTHVDWLGRDYTEIGAATVNTPKGF-----YVLESTYAQNAGLRPTILC 245
                                                                                                                                               155 --KEFILHDHV----REEAQAFLRGLRVNGSQPSTF--VGVHVRRGDXVHVMPNVWKGVV 206
                                                                                                                                                                                    246 VKGKLTKHDGTALSSEEMTAAPNAGWIVANNDPTTYYPVLVNFESNNYTYTGEAVEKGKI 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 19-208.
MEDLINE=20139694; PubMed=10673428;
Hallberg B.M., Bergfors T., Boeckbro K., Pettersson G., Henriksson G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li B., Nagalia S.R., Renganathan V., "Cellobiose dehydrogenase from Phanerochaete chrysosporium is encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A new scaffold for binding haem in the cytochrome domain of the extracellular flavocytochrome cellobiose dehydrogenase."; Structure 8:79-88(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Basidiomycota; Hymenomycetes; Homobasidiomycetes;
                                                                          -----IPWQNYHLNDWMEERYRHI-----PGHFVRFTGYPCSWTFYHH--LRPEIL-
                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cellobiose dehydrogenase precursor (EC 1.1.5.1) (CDH) (Cellobiose-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TO CELLOBIONOLACTONE.
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-!- COFACTOR: ONE FAD AND ONE HEME B.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE GMC
                                                                                                                                                                                                                         207 ADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGI 256
                                                                                                                                                                                                                                                             306 VRNHKFDINLTITGPGTNNPENPIT-----ESANLNVNCVVAAWKGV 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li B., Nagalla S.R., Renganathan V.; "Cloning of a cDNA encoding cellobiose dehydrogenase, hemoflavoenzyme from Phanerochaete chrysosporium."; Appl. Environ. Microbiol. 62:1329-1335(1996).
74 LARMNGRLAF--IPASMHNALAPIFRISLPVLHSDTAKK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Basidiomycota; Hymenomycete
Aphyllophorales; Corticiaceae; Phanerochaete.
NCBI_TaxID=5306;
                                                                                                                                                                                                                                                                                                                                                               773 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by two allelic variants.";
Appl. Environ. Microbiol. 63:796-799(1997).
                                                                                                                                                                                                                                                                                                                                                                 PRT;
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MEDLINE=97176414; PubMed=9023960;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97077226; PubMed=8919793;
                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last seq
15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phanerochaete chrysosporium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U46081; AAC49277.1; -.
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                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       quinone oxidoreductase).
CDH-1 AND CDH-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                           CDH_PHACH (001738; 000047;
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                                                                                                                                                                                                                                                                                                                      RESULT 15
CDH_PHACH
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12;

Gaps

78;

23 MIIQMSSGNIESPEMRRDSEQ-----HGNGELRGMFTINSIGRLGNQMG---EYAILEA 73

64; Conservative

Matches

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11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 TFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                397 T------INDNPNYKDHVF---GY--SAFDFLNGKRAGPVAIYLQTALA--RPNF 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     337 GDFSSSVGWPSSWINHAPYTSKLSSRLPSTDHPSTDGQRYLEQSFNVVSQLLKGQGYNQA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 ----NASRGDVVFAGNGIEGSPAKD-----FALLTQCNHTIMTIGTFG----IWAAYL 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    439 TEKTNVMVSNVVRNGSQILGVQFNDPTLGPNGFIPVTPKGRVILSAGAFGISRILFQSGI 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54; Gaps
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4.6%; Score 89; DB 1; Length 773;
Best Local Similarity 22.0%; Pred. No. 8.6;
Matches 49; Conservative 29; Mismatches 91; Indels
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HEMB LICAND.
FAD (ADP PART) (POTENTIAL).
54F721E779AA4D7B CRC64;
               qq
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Search completed: May 27, 2003, 15:07:13 Job time: 11.478 secs

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0920w3 mus musculu
07486 gorilla gor
077485 pan troglod
09tud3 gorilla gor
09tud5 pan troglod
029505 oryctolagus
077487 pongo pygma
09ttc7 hylobates l
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09r275 rattus norv
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070504 mus musculu
0920w2 mus spicile
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                                                                                                                                                                                                                                                                                                                                                                     1 MASAQVPFSFPLAHFLIFVF.....RSHFHLKAKGVTCYVAGRAF 380
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              671580 seqs, 206047115 residues
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Maximum Match 1008
Listing first 45 summaries
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Q55025
O35087
Q9JL27
Q9JL27
Q9JVW2
Q9JVW3
Q91VW3
Q77486
O77486
O77486
O77485
Q9TUD3
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Q9TUD3
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
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sp_phage:*
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240
                                                                      241 FRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIG 300
                                                                                   301 TFGIWAAYLAGGDIIYLANYILPDSPFLKVFKPBAAFLPEWVGIPADLSPLLKALTPACP 360
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Alpha 1,2 fucosyltansferase (Fragment).
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                          LIDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLERALDM
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Pred. No. 3.8e-164;
0; Mismatches 0;
                                                                                                                                                                                                                                353 AA
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EMBL, AF042743; AAC14695.1; -.
InterPro; IPR002516; GT_11.
FPM: PF01531; Glyco_transf_11; 1.
Glycosyltransferase; Transferase.
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SLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFT 180
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
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Mammalia; Eutheria; Rođentia; Sciurognathi; Muridae; Murinae; Rattus.
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328 LKVFKPEAAFLPEWVGIPADLSPLLKALTPACPRSHFHLKAKGVTCYVAGRAF 380
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                        Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Soejima M., Wang B., Koda Y., Kimura H.; "Two distinct rat GDP-L-fucose:b-D-galactoside 2-a-L-
                                                                                                                                                                                                             01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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Submitted (AUG-1997) to the
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TISSUE=COLON CANCER;
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Q9R275;
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Pfam; PF01531; Glyco_transf 11; 1.
Glycosyltransferase; Transferase.
SEQUENCE 347 AA; 39215 MW; 6160
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              Best_Local Similarity
Matches 317; Conserv
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                                                                                                                                                                                                                 Gaps
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"Molecular Cloning, Genomic Mapping, and Expression of Two Secretor Blood Group alpha (1.2)Fucosyltransferase Genes Differentially Regulated in Mouse Uterine Epithelium and Gastrointestinal Tract.";
D. Blol. Chem. 276:23748-23756(2001).

EMBL; AF214656; AAF45146.1;
                                                Bureau V., Marionneau S., Cailleau-Thomas A., Le Moullac-Vaidye B., Liehr T., Le Pendu J.;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                        'Comparison of the three rat GDP-L-fucose: beta-D-galactoside 2-
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                                                                                                                      InterPro; IPR002516; GT_11.
Pfam: PF01531; G1yco_transf_11; 1.
G1ycosyltransferase: Transferase.
SEQUENCE 354 AA; 39983 MW; 123E8C8379E8559E CRC64;
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                                                                                                                                                                                     Score 1878; DB 11;
Pred. No. 1.7e-162;
                                                                                   alpha L-fucosyltransferases FTA, FTB and FTC.";
Bur. J. Biochem. 268:1006-1019(2001).
EMBL; AF131238; AAD24469.1; -.
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MEDLINE=21316545; PubMed=11323419;
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InterPro; IPR002516; GT_11.
Pfm: PF01531; Glyco_tranf_11; 1.
Glycosytransferaes. Transferaes.
SEQUENCE 347 AA; 39243 MW; DD55
                                   MEDLINE=21099374; PubMed=11179967;
                                                                                                                                                                                       92.48;
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                                                                                                                  1 MASAQVPFSFPLAHFLIFVFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "GDP-fucose: beta-galactoside alphal,2-fucosyltransferase, MFUT-II,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and not MFUT-I or -III, is induced in a restricted region of the digestive tract of germ-free mice by host-microbe interactions and cycloheximide.";
                                                                                                                                                181 LHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDXVHVMPNVWKGVVADRGYLEKALDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 FRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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   Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lin B., Hayashi Y., Saito M., Sakakibara Y., Yanagisawa M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 294 TFGIWAAYLAGGDTIYLANYTLPDSPFLKIFKPAAAFLPEWMGIPADLSPLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 TFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK
                                                                Indels
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82.4%; Score 1674.5; DB 11;
89.8%; Pred. No. 5.3e-144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           347 AA
                                                          12; Mismatches
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EMBL; AF064792; AAC16887.1; -.
MGD; MGI:109374; Fut2.
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01-DEC-2001
01-DEC-2001
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                           RESULT 8
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                                       Q91VF0
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                        173
                                                                                                           234 FRARYSSPVEVVTSNGMAMCRENINTSLGDVVFAGNGIEGSPAKDFALLIQCNHTIMTIG 293
                                                        FRARYSSPVFVVISNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 FTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 WQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195 GLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTS 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 FLIFVFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGM 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFT
             LHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM
                                                                                                                                                                                                                                                                                                          Mus spicilegus (Steppe mouse).
Eukaryota: Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 255 NGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 NGMAWCRENINTSLGDVVFAGNGIEGSPAKDPALLTQCNHTIMTIGTFGIWAAYLAGGDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11; Length 321;
                                                                                                                                                7;
                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
20P-L-fucose:beta-pgalactoside 2-alpha-1-fucosyltransferase
2.4.1.69) (Fragment).
                                                                                                                                    TFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.2%; Score 1547.5; DB 11; Lengt 89.3%; Pred. No. 1.7e-132; ive 11; Mismatches 17; Indels
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36560 MW; 5B7D19BA6D4B5394 CRC64;
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InterPro; IPR002516; GT_11.
Fam: PF01531; Glyco_transf_11; 1.
Glycosyltransferase; Transferase.
NON_TER
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                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10103;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       255 NGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLIQCNHTIMTIGTFGIWAAYLAGGDT 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 FTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FLIFVFVTSTIIHLQQRIVKLQTLSEKEL-QAVQMSSPNAARTDMQQ-----SAKLQGI 53
                                                                                                                                                                                                                                                                                                                                                                                            Liu Y., Kitano T., Koide T., Shiroishi T., Moriwaki K., Saitou N.; "Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 FLIFVFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 GLRVNGSQPSTFVGVHVRRGDYVHVMPKVWKGVVADRGYLEKALDRFRARYSSPVFVVTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 NGMANCRENINTSLGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWANILAGGDT
                                                                                                                                                                                                                                             Euteleostomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11; Length 321;
                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
NCBL_TaxID=10090;
              091vF0;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Five Mus musculus subspecies.";
Submitted (FBB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB039114; BA8686391; --
EMBL; AB039115; BA8686391; --
EMBL; AB039116; BA8686401; --
EMBL; AB039116; BA8686411; --
EMBL; AB039119; BA8686431; --
EMBL; AB039120; BA8686431; --
EMBL; AB039120; BA8686441; --
EMBL; AB039120; BA8686441; --
EMBL; AB039120; BA8686441; --
EMBL; AB039121; BA8686441; --
EMBL; AB039121; BA8686441; --
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36516 MW; 0622D3BB503B72D1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.2%; Score 1547.5; DB 1.89.0%; Pred. No. 1.7e-132;
  AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Mismatches
321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPP002516; GT_11.
Pfam: PF01531; Glyco_transf_11; 1
Glycosyltransferase; Transferase.
NON_TER 321
SEQUENCE 321 AA; 36516 MW; 06:
                                                                                                                                                     (EC 2.4.1.69) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=VARIOUS STRAINS;
Liu Y., Kitano T., Koid
                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 292; Conserv
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us-10-040-863-8.rspt

5

Gaps

Indels

DB 6; Length 343;

49

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Koda Y., Tachida H., Soejima M., Takenaka O., Kimura H.; "The old origin of a null allale set38 of the human ABO-secretor type alpha(1,2) fucosyltransferase gene (FUT2)."; submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STSKALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAPIPAQMHSTLAPIFRI 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-95181460; FubMed=7875235;
Kelly R.J., Rouquier S., Giorgi D., Lennon G.G., Lowe J.B.;
Sequence and expression of a candidate for the human secretor blood group alpha(1,2) fucceyltansferase gene (FUT2).";
J. Biol. Chem. 270:4640-4649(1995).
EMBL; AB015635; BAA31128.1;
InterPro; IPR02516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Glycosyltransferase; Transferase.
SEQUENCE 343 AA; 38973 MW; 894E28BD74AEBFBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 SLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFT 180
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"Sequence and expression of a candidate for the human secretor blood
group alpha(1,2) fucosyltansferase gene (FUT2).";
J. Biol. Chem. 270:4640-4649(1995).

EMBL; AB015634; BAA31127.1;
Interpro, IPR002515; GT_11.
Glycosyltransferase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                             1 MASAQVPFSFPLAHFLIFVFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                           290 TFGIWAAYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLK 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 TFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butel
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38999 MW; B849D7E152852081 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08, Last sequence update)
20, Last annotation update)
                                                                                                                                                                                                                                                            73.8%; Score 1499.5; DB 6; 78.5%; Pred. No. 4.4e-128; Wismarches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA.
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                                                                                                                                                                                                                                                                                                                                          Matches 277; Conservative
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Best Local Similarity
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01-MAR-2002
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                                                                                                                                                                                                                                                            STRAIN=NJI/MSF;
Liu Y., Kitano T., Koide T., Shiroishi T., Moriwaki K., Saitou N.;
"Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1] SEQUENCE FROM N.A. Soejima M., Takenaka C., Kimura H.; Koda Y., Tachida H., Soejima M., Takenaka C., Kimura H.; The old origin of a null allele se428 of the human ABO-secretor type alpha(1,2) fucosyltransferase gene (FUT2)."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTINSIGRIGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDIAKKIP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 FTINSIGREGNOMGEYATLFALARMNGRLAFIPESMHNALAPIFRISLPVLHSDIARRIP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FLIFVFVTSTIIHLQQQIVKLQTLSEKEL-QAVQMSSPNAARTDMQQ-----SAKLQGI 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 FLIFVFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGM 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 NGMAWCRENINTSLGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
NCBI_TaxID=9593;
                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.4%; Score 1532.5; DB 11; Length 321; llarity 88.4%; Pred. No. 4e-131; Conservative 13; Mismatches 18; Indels 7;
  01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase
2.4.1.69) (Fragment).
                                                                                                                                                                                                                                                                                                                                     Five Mus musculus subspecies,";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AB039122; BAB6666.1;
InterPro; IRR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
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321 AA; 36464 MW; FF5304CD150F774A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294 IYLANYTLPDSPFLKIFKPAAAFLPEWM 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
Alpha(1,2) fucosyltransferase.
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                                                                                                           musculus (Mouse)
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                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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SEQUENCE
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     HER REPARENTED TO THE PROPERTY OF THE PROPERTY
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300

289

Euteleostomi;

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181 LHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM 240
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                                                                                                                                                                                     338
                                                                                                                                                                                     PRT;
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EMBL, AF080604; AAF14066.1; -.
InterPro; IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
                                                                                                                                                                                                                                             fucosyl transferase.
                                                                                                                                                                                                                                                                   Pan troglodytes (Chimpanzee)
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                                                                                                                                                                                     PRELIMINARY;
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01-MAR-2002
Alpha (1,2)
FUT2.
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Q9TUD5
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Q29505
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                                                                                                    SLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFT 180
                                                                                                                                                                                 LHDHVREEAQAFLKGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM 240
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                                                                                       61 RDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRI 120
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                        Gaps
                                                                 1 MLVVQMPFSFPVAHFILFVFTVSTIFHVQQRLAKIQAM--WELPV------QIPVLA 49
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                                                                                                                                                  1 MASAQVPFSFPLAHFLIFVFVTSTITHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMR
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Gorilla gorilla (gorilla).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Gorilla.
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                                                                                                                                                                                                                                                                                      290 TFGIWAAYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWMGIAADLSPLLK 342
                                                                                                                                                                                                                                                                          301 TFGIWAAYLAGGDIIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 6; Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Apoil P.-A., Roubinet F., Despiau S., Mollicone R., Oriol R., Blancher A.;
                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 343 AA; 39001 MW; A753375D47AE8C8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
No. 1e-127;
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                    31; Mismatches
                                                                                                                                                                                                                                                                                                                                                           343 AA
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          Pred.
                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20188794; PubMed=10723735;
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EMBL; AF080606; AAF14068.1;
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Pfam; PF01531; Glyco_transf_11; 1.
Transferase.
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        78.2%;
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                     Conservative
                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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        Best Local Similarity
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01-MAR-2002
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                   Matches
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Q9TUD3
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170 LHDHUYREEAQKFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDM 229
                                                                         241 FRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 LGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVL 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 VPFSFPLAHFLIFVFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Evolution of alpha2-Pucosyltransferase genes in primates: relation between an intronic Alu-Y element and red cell expression of ABH
                                                                                                        230 FRARYSSPIFVVTSNGMAMCRENIDISHGHUNTHHHHHHHHHHHHHHHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTLMTIGTFGIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                              290 TFGIWAAYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLK 342
                                                                                                                                                                                              301 TFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.3%; Score 1488.5; DB 6; Length 338; 78.7%; Pred. No. 4.3e-127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-20188794; Pubmed-10723735;
Apoll P.-A., Roubinet F., Desplau S., Mollicone R., Oriol R.,
Blancher A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               290 AAYLIGGDTIYLANYILPDSPFLKIFKPEAAFLPEWMGIAADLSPLLK 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306 AAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              338 AA; 38428 MW; E7FABAOFF1BC95F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32;
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                                                                                                                                                                                                                              HILDSH: S., KOJIMAN, KANGZAWA I., TSUJI S.;
HILDSH: S., KOJIMAN, KANGZAWA I., TSUJI S.;
HUCOSE: DELO CONING AND GENESSION OF a third type of rabbit GDP-L-fucose: Dela Chem. 27:116975-16981(1996)
J. BIOL. Chem. 27:116975-16981(1996)
J. BIOL. Chem. 27:116975-16981(1996)
J. FUNCTION: CREATES A MEMBRANE-ASSOCIATED PRECURSOR OLIGOSACCHARIDE FUCALPHA((1,2)GALBETA-) CALLED THE HANTIGEN WHICH IS AN ESSENTIAL SUBSTRATE FOR THE FINAL STEP IN THE MEMBRANE-ASSOCIATED A AND B ANTICEN SYNTHESIS PATHWAY. HAND SE ENZYMES PUCOSYLATE THE SAME ACCEPTOR SUBSTRATES BUT EXHIBIT DIFFERENT KM VALUES.
-!-CATALYTIC ACTIVITY: GDP-L-FUCOSE + BETA-D-GALACTOSYL-R = GDP + ALPHA-L-FUCOSYL-1, 2-BETA-D-GALACTOSYL-R = GDP +
                           01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MR-2002 (TrEMBLrel. 20, Last annotation update)
01-MR-2002 (TrEMBLrel. 20, Last annotation update)
Galactoside 2-L-fucosyltransferase 3 (EC 2.4.1.69) (Secretor blood group ALPHA--L-fucosyltransferase) (GDP-L-fucose:beta-D-galactoside 2-ALPHA-L-fucosyltransferase) (ALPHA(1,2)FT) (Fucosyltransferase 3);
01yctolagus cuniculus (Rabbit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 PTSQRAPSRPLGGMWTINAMGRLGNQMGEYATLYALAKENGRPAYIPAQMHSTLAPIFRI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.
-!- TISSUE SPECIFICITY: ADULT GASTROINTESTINAL TRACT AND COLON.
-!- MISCELLANEOUS: THERE ARE THREE GENES (FOT1, FOT2 AND FOT3) WHICH ENCODE GALACTOSIDE 2-L-FUCOSYLTRANSFERASE IN RABBIT. THEY ARE EXPRESSED IN A TISSUE-SPECIFIC MANNER.
-!- SIMILARITY: STRUCTURAL SIMILARITY WITE THE OTHER MAMMALIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 LHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIG
                                                                                                                             Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LUMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GICNAC. ) (POTENTIAL).
N-LINKED (GICNAC. .) (POTENTIAL).
N-LINKED (GICNAC. .) (POTENTIAL).
746F7007309862A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X91269; CAA62669.1; -
InterProx; PR005216; GT_11.
Pfam; PF01531; Glycoc transf.11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 6; Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.5e-127;
 347 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.3%; Score 1488.5; 78.2%; Pred. No. 4.5e
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=GASTROINTESTINAL TRACT;
MEDLINE=96279281; Pubmed=8663168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                347 LT
192 N-
286 N-
312 N-
39469 MW;
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 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 3
192 1
286 2
312 3
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                                                                                                                                                             NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276;
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CARBOHYD
SEQUENCE
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               029505;
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029505
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SEQUENCE FROM N.A. Socjima M., Takenaka O., Kimura H.; Koda Y., Tachida H., Socjima M., Takenaka O., Kimura H.; "The old origin of a null allele se428 of the human ABO-secretor type alpha(1,2), fucosyltransferase gene (FUT2)."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kelly R.J., Rouquier S., Giorgi D., Lennon G.G., Lowe J.B.;
"Sequence and expression of a candidate for the human secretor blood group alpha(1,2) fucceyltansferase gene (FUT2).";

EMBL, ABO15636; BAA31129.1;
InterPro; IPRO02516; GT_11.
Pfam, PFO1531; Glyco_transf_11; 1.

Glycosyltransferase; Transferase.
SEQUENCE 343 AA, 38973 MW; 2BD4D2A9704E4A0C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       230 FRARYSSPIFVVTSNGMAWCQENIDTSHSDVVFAGDGIEGSPAKDFALLTQCNHTIMTIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 SLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFT
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                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pongo.
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                             294 TEGIWAAYLIGGDIYLANYTLPDSPFLKIFKPEAAFLPEWVGINADLSPLLK 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 TFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 353
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77.9%; Pred. No. 5.4e-127;
... wismatches 36; Indels
                                                                                                                                                                                                                                       (TrEMBLrel. 08, Created)
(TrEMBLrel. 08, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
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ne : 43.5157 secs
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                                                                                                                                                                                                                                                                                                                                  Alpha(1,2) fucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                             Pongo pygmaeus (Orangutan)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 77.9 Matches 275; Conservative
                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                              01-NOV-1998 (TrEMBLrel. 01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9600;
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01-NOV-1998
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Job time
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May 27, 2003, 15:01:52 ; Search time 38.17 Seconds (without alignments) 1932.533 Million cell updates/sec
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1 STITHLQQRIVKLQPLSEKE.....RSHFHLKAKGVTCYVAGRAF 358
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                          671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                       US-10-040-863-8_COPY_23_380
                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: sp_archea:*
2: sp_archea:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
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Seguence:
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Maximum DB :
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		Description	44 rattus norv	25 rattus norv	rattus	rattus					w3 musculu	6 dorilla dor	5 pan trodlod		3 gorilla gor			
	í	Descr	091k44	055025	035087	09r275	091127	070504	0920w2	091vf0	0920	O77486 ac	09tud	077485	09tud	029505	07748	099450
SUMMARIES	ć	1.D	Q9JK44	055025	035087	Q9R275	Q9JL27	070504	0920W2	Q91VF0	Q920W3	77486	99TUD5	77485	9TUD3	029505	277487	299450
		- !	11	11	11	11	11	11	11	11	11	9	9	9	9	9	9	4
	, ; ;	матсл Lengtn DB	380	353	354	354	347	347	321	321	321	343	338	343	343	347	343	332
	& Query Match	March	100.0	98.7	92.2	92.0	81.4	81.2	78.5	78.5	77.7	74.0	73.8	73.8	73.8	73.5	73.4	73.1
	0 0 0	9700c	1921	1896	1772	1767	1563.5	1559.5	1508.5	1508.5	1493.5	1421.5	1418.5	1418.5	1417.5	1412.5	1410.5	1403.5
	Result No		⊣	7	m	4	Ŋ	9	7	æ	6	10	11	12	13	14	15	16

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Gaps

STIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR 60

100.0%; Score 1921; DB 11; Length 380; llarity 100.0%; Pred. No. 1.2e-166; Conservative 0; Mismatches 0; indels 0;

Query Match Best Local Similarity Matches 358; Conserv

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121 WMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKBFTLHDHVREEAQAFLRGLRVNGSQ 180

5	nc7 hvlobates	5000 500	O14338 home sapian	attus	08.00	us muscul	anw sn	caca f	lemuı	llithrix	caca	caca fas	Stai	us II	us muscul	Sn	3	s taurus	1,6	rilla q	lobates	caca m	obu	mo sapie	caca fa	mo sapie	n trogl	sapie	
7712	TTC7	920T3	4338	9WUE6	920T2	920T4	91V73	Q9TSL5	TTC9	TIDO	TUD1	N266	TTY3	9JL28	97327	920W5	920W4	TTY7	TUE6	TUD4	TUE7	TUD2	N270	WXB6	2	150	ľUD	150	ALIGNMENTS
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17	18	19	20	21	22	23	24	25	26	27	28	53	30	33	32	33	34	35	36	37	38	33	40	4 ⊥	42	43	44	45	

RESULT Q9JK44	1
A B	Q9JK44 PRELIMINARY; PRT; 380 AA. Q9JK44;
DI	01-OCT-2000 (TrEMBLrel, 15, Created)
DI	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DŢ	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE	Alpha 1-2 fucosyltransferase.
SO	Rattus norvegicus (Rat).
ပ္ပ	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
8	Mammalia; Eutheria; Rodentia; Sciuroquathi; Muridae; Murinae; Rattus.
XO	NCBI_TaxID=10116;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=FISCHER;
RA	Sherwood A.L., Stroud M.R., Levery S.B., Holmes E.H.;
RT	"An amino acid region at the N-terminus of rat hepatoma H35 cell GDP-
RŢ	fucose: GM1 alpha 1-2 fucosyltransferase is required for optimum enzyme
RT	activity and interaction with lipids.";
RL	Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AF264005; AAF72200.1;
DR	InterPro; IPR002516; GT_11.
DR	Pfam; PF01531; Glyco_transf_11; 1.
Κ₩	Glycosyltransferase; Transferase.
SO	SEQUENCE 380 AA; 42742 MW; 920692C96689C05C CRC64;

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BUFFALO RAT:
MEDINE=98342055; PubMed=9675030;
MEDINE=98342055; PubMed=9675030;
Sherwood A.L., Holmes E.H.;
"Cloning and expression of the catalytic domain from rat hepatoma H35 cell GDP-fucose: GMI alpha 1-->2fucosyltransferase, an enzyme which is activated during early stages of chemical carcinogenesis in rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MR-2020 (TrEMBLrel. 20, Last annotation update)
Alpha 1,2 fucosyltransferase (Fragment).
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
143 WMEBRYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQ 202
                                                                                                                           240
                                                                                                                                                              263 NINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTL 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 YRHIPGHFVRFIGYPCSWTFYHHLRPEILKBFTLHDHVREEAQAFLRGLRVNGSQPSTFV 185
                                                                                                                                                                                                                                                              241 NINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTL 300
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                                                                                                                                                                                                                                                                                                                                                                                                                 PDSPFLKVFKPEAAFLPEWVGIPADLSPLLKALTPACPRSHFHLKAKGVTCYVAGRAF 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVHVRRGDYVHVMFNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS
                                                                                                                   PSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRE
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Arch. Blochem. Blophys. 355:215-221(1998).
BMBL,
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nes 353; Conservative
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRE · 240
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Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STITHLOORIVKLOPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 STITHLOORIVKLOPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 PSTFVGVHVRRGDYVHVMPNVMKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                              fucosyltransferase genes.";
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB006138; BAA21742.1;
Interpro; IPR002516; GT_11;
Pfam; PF01531; Glyco_transf_11; 1.
Glycosyltransferase; Transferase.
SEQUENCE 354 AA; 39995 MW; 8636444888215BA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                Socjima M., Wang B., Koda Y., Kimura H.;
"Two distinct rat GDP-L-fucose:b-D-galactoside 2-a-L-
                                                                           01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Alpha 1,2-fucosyltransferase.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92.2%; Score 1772; DB 11;
100.0%; Pred. No. 4.2e-153;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323 PDSPFLKVFKPEAAFLPEWVGIPADLSPLLK
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                                                      05, Created)
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Alpha I,2-fucosyltransferase,
FIB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 331; Conservative
  PRELIMINARY;
                                                      01-JAN-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
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Q9R275;
<del>03</del>5087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263 NINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTL 322
                                                                                                                                                                                                                                                                                                                                                                                                                                 61 LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
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                                                                                                                                                                                                                                                                                                                                                                      Domino S.E., Zhang L., Lowe J.B.;
"Molecular Cloning, Genomic Mapping, and Expression of Two Secretor Blood Group alpha (1,2)Pucosyltransferase Genes Differentially J. Biol. Chem. 276:23748-23756(2001).
                                                                                                                                                                                                                                                                                                                                         STITHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WMEERYRHIPGHFVRFTGYPCSWTFYHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQ
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Bureau V., Marionneau S., Cailleau-Thomas A., Le Moullac-Vaidye
                                                                                                                                                                                                                                                                                              0;
                  Liehr T., Le Pendu J.;
"Comparison of the three rat GDP-L-fucose: beta-D-galactoside Jalpa-L-fucosyltransferases FTA, FTB and FTC.";
Eur. J. Biochem. 268:1006-1019(2001).
EMBL; AF131238; AAD24469.1;
InterPro: IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Glycosyltransferase; Transferase.
SEQUENCE 354 AA; 39983 MW; 123E8C8379E8559E CRC64;
                                                                                                                                                                                                                                                    354;
                                                                                                                                                                                                                                             DD5F441046CC8E79 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Alpha(1,2)fucosyltransferase FUT2 (EC 2.4.1.69).
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InterPro; IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
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61 LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                          PSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRE 240
                                                                                                                                              LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and not MFUT-I or 'III, is induced in a restricted region of the digestive tract of germ-free mice by host-microbe interactions and cycloheximide.";
                                      196 PSTFVGVHVRRGDYVHVMPKVWKGVVADRGYLEKALDRFRARYSSPVFVVTSNGMAWCRE
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
STITHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. TRACT;
STRAIN-ERR ITSSUE-GASTROINIESTINAL TRACT;
MEDILNE-20471982: pubMed=11018479;
Lin B., Hayashi Y., Saito M., Sakakibara Y., Yanagisawa M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          616CCB11581C4179 CRC64;
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MBBL; ARCO64792; ARCLE6887.1; -.
MGI:L109374; Futc.
InterPro; IPR002516; GT_11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDSPELKIFKPAAAFLPEWMGIPADLSPLLK 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
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SEQUENCE
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Q920W3
  PAPER SOLUTION OF THE 
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                                PSTFVGVHVRRGDYVHVMPKVWKGVVADRGYLEKALDRFRARYSSPVFVVTSNGMAWCRE 255
                                                                                                            181 PSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRE 240
                                                                                   241 NINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 WMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu Y., Kitano T., Koide T., Shiroishi T., Moriwaki K., Saitou N.; "Conspicuous Differences among Gene Genealogies of 21 Nuclear Gene.
Five Mus musculus subspecies.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus spicilegus (Steppe mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
NCBI_TaxID=10103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.5%; Score 1508.5; DB 11; Length 321; 89.1%; Pred. No. 3.7e-129; Live 11; Mismatches 17; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase
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36560 MW; SB7D19BA6D4B5394 CRC64;
                                                                                                                                                                                                                                                                                                                                 321 AA.
                                                                                                                                                                                               316 PDSPFLKIFKPAAAFLPEWMGIPADLSPLLK 346
                                                                                                                                                                        PDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 331
                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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FUT2.
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321 AA;
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285; Conserv
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SEQUENCE
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Best Local S:
Matches 285,
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Q920W2;
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091VF0
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STRAIN-VARIOUS STRAINS,

A Liu Y., Kitano T., Koide T., Shiroishi T., Moriwaki K., Saitou N.;

Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of Five Mus musculus subspecies.

Liu Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AB039115; BAB66338.1; -..

REMBL; AB039115; BAB6639.1; -..

REMBL; AB039116; BAB6640.1; -..

REMBL; AB039118; BAB6644.1; -..

REMBL; AB039118; BAB6644.1; -..

REMBL; AB039121; BAB6644.1; -..

REMBL; AB039121; BAB6644.1; -..

REMBL; AB039121; GT_11; -..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 WMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa; Chordata, Craniata; Vertebrata, Buteleostomi:
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0920W3;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
6DP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase (EC
FUT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.5%; Score 1508.5; DB 11; Length 321; 88.8%; Pred. No. 3.7e-129; ive 12; Mismatches 17; Indels 7;
                 091VF0;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DTN-2002 (TrEMBLrel. 21, Last annotation update)
GDP-L-fucose:Deta-D-galactoside 2-alpha-1-fucosyltransferase
(EC 2.4.1.69) (Fragment).
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     AA
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321
  PRT;
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NON_TER 1 1
NON_TER 321 321
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Matches 284; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                           Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                321 AA;
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Gaps

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181 PSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRE 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQ 180
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                                                                                                                                                                                                                                                                                                                                               1 STITHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 STIFHVQQRLAKIQAM--WELPV-----QIPVLASTSKALGPSQLRGWWINAIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                      DB 6; Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.8%; Score 1418.5; DB 6; Length 338; 79.5%; Pred. No. 6.4e-121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20198794; PubMed=10723735;
Apoil P.-A., Roubinet F., Despiau S., Mollicone R., Oriol
Blancher A.;
                                                                                                                                                                                                               74.0%; Score 1421.5; DB 6; Length.
79.8%; Pred. No. 3.5e-121;
Live 25; Mismatches 31; Indels
                                                                                                                                                            894E28BD74AE8FBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               338 AA; 38428 MW; E7FABA0FF1BC95F9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            312 PDSPFLKIFKPEAAFLPEWTGIAADLSPLLK 342
J. Biol. Chem. 270:4640-4649(1995).
EMBL; AB015635; BAA31128.1;
Interpro: IPR002516; Gr_11.
Pfam; PF01531; Glyco_transf_11; 1.
Glycosyltransferase; Transferase.
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EMBL, AF080604; AAF14066.1; -.
InterPro: IPR002516; GT_11.
Pfam: PF01531; Glyco_transf_11; 1.
Transferase.
                                                                                                                                                         38973 MW;
                                                                                                                                                                                                               Query Match 74.08
Best Local Similarity 79.89
Matches 264; Conservative
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                                                                                                                                                            343 AA;
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                                                                                                                                                                                                               Liu Y., Kitano T., Kolde T., Shiroishi T., Moriwaki K., Saitou N.; "Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of Five Mus musculus subspecies.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE FROM N.A.

Koda Y., Tachida H., Soejima M., Takenaka O., Kimura H.;

Koda Y., Tachida H., Soejima M., Takenaka O., Kimura H.;

"The old origin of a null allele se428 of the human ABO-secretor type alpha(1,2) fucosyltransferase gene (FUT2).";

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 NINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTL 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 STIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 PSTFVGVHVRRGDYVHVMPKVWKGVVADRGYLEKALDRFRARYSSPVFVVTSNGMAMCRE
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                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Gorilla.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11; Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Indels
                                                                                                                                                                                                                                                                            Five Mus musculus subspecies.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AB039122; BAB68646.1; -.
InterPro; IFR00216; GT_11.
Pfam: PF01531; Glyco_transf_11; 1.
Glycosyltransferase; Transferase.
NON_TER 321 321
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01-NVV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.7%; Score 1493.5; DB 1
88.1%; Pred. No. 8.7e-128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            343 AA
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Matches 282; Conservative
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                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                               NCBI_TaxID=10090;
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                                                                                                                                                                                         STRAIN-NJL/MSF;
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Similarity
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Best Local Simi
Matches 263;
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Q29505;
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Q29505
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             180
                                                           NINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTL 300
                                                                                                                                                         61 LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSIFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRE 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-5588146; pubMed=7876235; Kelly R.J., Rouquier S., Giorgi D., Lennon G.G., Lowe J.B.; Kelly R.J., Rouquier S., Giorgi D., Lennon G.G., Lowe J.B.; Sequence and expression of a candidate for the human secretor blood group alpha(1,2) fucosyltansferase gene (FUT2)."; BMBL; AB015634; BAA31127.1; Interpret 1PR002516; G_L11.
Interpret 1PR002516; G_L11; Glyco_transf_l1; l. Glycosyltransferase; Transf_l1; l. Glycosyltransferase: Transf_erase.
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                                             WMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQ
                                                                                                                     PGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSPIFVVTSNGMAWCRE
                                                                                               PSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRE
                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                        Hominidae; Pan
                                                                                                                                                                                                                                                                                                                                                              Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                   01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                               343 AA
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Alpha(1,2)fucosyltransferase.
FUT2.
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Best Local Similarity 79.5
Matches 263; Conservative
                                                                                                                                                                                                                                                                               PRELIMINARY;
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241 NINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTL 300
                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Evolution of alpha2-Fucosyltransferase genes in primates: relation between an intronic Alu-Y element and red cell expression of ABH antigens.";
Mol. Biol. Evol. 17:337-351(2600).
EMBL; AF080606; AAF14068.1; -.
Pfam; PF01531; Glyco_transf_l1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotá; Metazoá; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Length 343;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.8%; Score 1417.5; DB 6; 79.5%; Pred. No. 8.1e-121; iive 26; Mismatches 31;
                                                                                                                                                                                                                                                                      343 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA
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                                                                                          PDSPFLKVFKPEAAFLPEWVGIPADLSPLLK 331
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                                                                                                                                        PDSPFLKIFKPEAAFLPEWMGIAADLSPLLK
                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=ALEXIS;
MEDLINE=20188794; Pubmed=10723735;
                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Last
01-MAR-2002 (TrEMBLrel. 20, Last
Alpha (1,2) fucosyl transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gorilla gorilla (gorilla)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                    PRELIMINARY;
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"Molecular cloning and expression of a third type of rabbit GDP-L-
fucose.beta-D-galactoside 2-alpha-L-fucosyltransferase.";

J. Biol. Chem. 27:16975-16981(1996).

-!- FUNCTION: CREATES A MEMBRANE-ASSOCIATED PRECURSOR OLIGOSACCHARIDE
FUC-ALPHA((1,2)GALBETA-) CALLED THE H ANTIGEN WHICH IS AN
ESSENTIAL SUBSTRATE FOR THE FINAL STEP IN THE MEMBRANE-ASSOCIATED
A AND B ANTIGEN SYNTHESIS PATHWAY. H AND SE ENZYMES FUCOSYLATE THE
SAME ACCEPTOR SUBSTRATES BOT EXHIBIT DIFFERENT KM VALUES.

-!- CATALYTIC ACTIVITY: GDP-L-FUCOSE + BETA-D-GALACTOSYL-R = GDP +
ALPHA-L-FUCOSYL-1, 2-BETA-D-GALACTOSYL-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLND 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIDASRGDVVFAGNGLESSPAKDFALLTQVNHTVMTIGTFGIWAAYLTGGDTIYLANYTL 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- TISSUE SPECIFICITY: ADULT GASTROINTESTINAL TRACT AND COLON.
-!- MISCELLANEOUS: THERE ARE THREE GENES (FUT1, FUT2 AND FUT3) WHICH ENCODE GALACTOSIDE 2-L-FUCOSYLTRANSFERASE IN RABBIT. THEY ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 STITHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGR 60
           Galactoside 2-L-fucosyltransferase 3 (EC 2.4.1.69) (Secretor blood group ALPHA-2-fucosyltransferase) (GDP-1-fucose:beta-D-galactoside 2-ALPHA-1-fucosyltransferase) (ALPHA(1,2)FT) (Fucosyltransferase 3 Oryctolagus cuniculus (Rabbit) (Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria: Lagomorpha: Leporidae: Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                             -!- PATHWAY: GLYCOSYLATION.
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN, MEMBRANE-BOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSTFVGVHVRRGDYVRVMPQVWKGVVADRGYLEQALDWFRARYRSPVFVVTSNGMAWCRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LUMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
746F7007309862A5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.5%; Score 1412.5; DB 6; Length 347; 79.8%; Pred. No. 2.3e-120;
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InterPro; IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 2.3e-120;
5: Mismatches 35; Indels
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01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXPRESSED IN A TISSUE-SPECIFIC MANNER.
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                                                                                                                                                                                               MEDLINE=96279281; PubMed=8663168;
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DOMAIN
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347 AA;
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                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                      NCBI_TaxID=9986;
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Koda Y., Tachida H., Soejima M., Takenaka O., Kimura H.;

"The old origin of a null allele se428 of the human ABO-secretor type
alpha(1,2) fucosyltransferase gene (FUT2).";

Submitted (JUN-1998) to the EMBL/Genbank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                       MEDLINE=95181460; PubMed=7876235; Kelly R.J., Roughler S., Glorgi D., Lennon G.G., Lowe J.B.; Kelly R.J., Roughler S., Glorgi D., Lennon G.G., Lowe J.B.; Sequence and expression of a candidate for the human secretor blood group alpha(1,2) fucosyltansferase gene (FUT2)."; J. Balol. Chem. 270.4846-4669(1995).
InterPro., IPR002516; GI_11.
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                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
NCBI_TaxID=9600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.4%; Score 1410.5; DB 6; Length
79.2%; Pred. No. 3.5e-120;
ive 27; Mismatches 31; Indels
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Glycosyltransferase; Transferase.
SEQUENCE 343 AA; 38973 MW; 2BD4
                                 PRT;
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FUT2.
                                                                                                                                              Pongo pygmaeus (Orangutan).
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                                 PRELIMINARY;
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01-NOV-1998 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	AT042 AF264 AF264 AR131 AR030	p mRNA linear ROD 01-MAY-2001 cosyltransferase mRNA, partial cds. Craniata: Vertebrata: Euteleostomi; Sciurognathi; Muridae: Murinae;
SUMMARIES	AF04274 AF26405 AF26405 AF26405 AB006138 AB006138 AF214656 AF0647374 AF064792 AF039115 AB039116 AB039119 AB039119 AB039119 AB039119 AB039119 AB039119 AB039120 AB039120 AB039120 AB039212 AF111239 AB039212 AF111239 AB039210 AB039210 AB039206 AF136895 AF214658 AF21668	1,2 fu 1,2 fu 1,2 fu data; entia; of the
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CIGICCCCACTCCTTAAGGCAITAACACCAGCCTGTCGTCGGTCCCACTTCCACCTCAAG 1020
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Biochemistry 40 (19), 5708-5719 (2001)
                                                                                                                                                   CCAGTCTTCGTGGTTACAAGCAACGGTATGGCCTGGTGCCGGGAGAACATTAATGCTTCC
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2 (bases 1 to 1149)
Sherwood,A.E. and Holmes,E.H.
Direct Submission
Submitted (05-MAY-2000) Molecular Medicine, Northwest Hospital,
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 CCAGTCTTCGTGGTTACAAGCAACGGTATGGCCTGGTGCCGGGAGAACATTAATGCTTCC
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Rattus norvegicus alpha 1-2 fucosyltransferase mRNA,
AF264005
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Sciurognathi; Muridae;
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/protein_id="AAF72200.1"
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/codon_start=1
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/db_xref="taxon:10116"
/cell_line="Reuber H35
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Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
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RGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDT
AKKIPWQNYHLNDWMBERYRHIPGHFVRFTGYPCSWFFYHHLRPEILKEFTLHDHVRE
                                                                                                                                                                                                                                                                                                                                                                                                                    EAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWRGVVADRGYLEKALDNFRARY
SPVFVYTSROMAMCRENIRASRGDVVFAGNGIEGSPAKDFALLTQCHHTIMTIGTFG
IMAAYLAGGDTIANYTLPDSPFLKVFKPFBAFLFEWVGIPADLSFLKALTPACPR
SHFHLKARGVTCYVAGRAF"
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                                                                                                                                                   Northwest Hospital
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H35 cell GDP-fucose:GMI alpha 1-->2fucosyltransferase, an enzyme which is activated during early stages of chemical carcinogenesis
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Submitted (13.3AM-1998) Cell Surface Biochem., Nort
120 Northgate Plaza, Suite 230, Seattle, WA 98125,
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                   /product="alpha 1,2 fucosyltransferase"
/protein_id="AAC14695.1"
/db_xref="G1:2801825"
                               in rat liver
Arch. Biochem. Biophys. 355 (2), 215-221 (1998)
98342056
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                                                                                                                                                                                                      /organism="Rattus norvegicus"
/strain="Buffalo rat"
/db_xref="taxon:10116"
/cell_line="hepatoma Reuber H35"
<1.1062
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                                                                                                2 (bases 1 to 1068)
Sherwood, A.L. and Holmes, E.H.
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922 TACCTGGCAGGTGGTGATACCATCTACTTAGCCAACTACACCTTCCGGATTCTCCGGTTC 981
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/db_xref="taxon:10116"
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<211. .>1275
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AF131238.1 GI:4580672
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/gene="FTB"
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         /translation="MASAQVPFSFPLAHFLIFVFVTSTITHLQQRIVXLQPLSEKELP
MTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALAFMNGR
LAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTG
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GIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPE
AAFLPEWVGIPADLSPLLKALTPACPRSHFHLKAKGVTCYVAGRAF"
                                            YPCSWIFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVH
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/db_xref="GI:8099677
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/product-"alpha 1,2-fucosyltransferase B"

protein_id="AAD24469.1"

/db_xref="GI:4488673"

/translation="MASAQVPFSFPLAHFLIFVFVTSTITHLQQRIVKLQPLSEKELP

/translation="MASAQVPFSFPLAHFLIFVFVTSTITHLQQRIVKLQPLSEKELP
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YPCSWTFYHHLRPEIIKEFTLHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDXVH
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Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Liehr.T. and Le Pendu,J.
Comparison of the three rat GDP-L-fucose:beta-D-galactoside
2-alpha-L-fucosyltransferases FTA, FTB and FTC
Eur. J. Biochem. 268 (4), 1006-1019 (2001)
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Direct Submission
Submitted (25-FEB-1999) INSERM U419, Instit
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WPNVWRGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAMCRENINASRGDVVFAGN
GIEGSPBARDFALLYGCHTTHYTIGTFGIMAAYLAGGDTIYLANYTLPDSSPELKVFKPE
AAFLPEWVGIPADLSPLLKH"
  ROD 05-FEB-1999
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Submitted (04-AUG-1957) Yoshiro Koda, Kurume University, School of
Submitted, Department of Forensic Medicine, Asahimachi 57, Kurume,
Medicine, Department of Forensic Medicine; Asahimachi 57, Kurume,
Fukuoka 810, Japan (E-mail:ykoda@med.kurume-u.ac.jp,
Tel:0942-31-754, Fax:0942-31-7700)
Location/Qualifiers
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                 Rattus norvegicus FTB mRNA for alpha 1,2-fucosyltransferase, complete cds.
AB006138
                                                                                       AB006138.1 GI:2317265
FTB: alpha 1,2-fucosyltransferase.
Rattus norvegicus colon cancer cell_line:RCN-9 cDNA to mRNA.
Rattus norvegicus
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/protein_id="BAA21742.1"
/db_xref="G1:2317266"
                                                                                                                                                                                                                                                                                      Soejima,M., Wang,B., Koda,Y. and Kimura,H.
Two distinct rat GDP-L-fucose:b-D-galactoside
2-a-L-fucosyltransferase genes
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Pred. No. 2.9e-266;
); Mismatches 2;
  mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Rattus norvegicus"
/db_xref="taxon:10116"
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/cell_line="RCN-9"
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 63 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
TITLE
JOURNAL
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CIGICCCCACICCIIAAGGCATTAACACCAGCCIGICCTCGGTCCCACTICCACCICAAG 1020
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Muzny,D.M., Adans,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaria,J., Benton,J., Binage,K., Blankenburg,K., Bonnin,D.,
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GGTGTCCATGTGCGCCGAGGGGACTATGTGCATGTCATGCCTAATGTGTGGAAGGGCGTG
                                                                                                                                                                                                                                                                                                                                                                           GTGGCTGACCGGGGTTACCTGGAAAAGGCCCTGGATATGTTCCGGGCACGCTATTCATCT
                                               TACCGCCACATTCCGGGACACTTTGTGTGCGCTTCACGGGATACCCGTGCTCCTGGACCTTC
                                                                                                                                                                              421 TACCACCACTGCGCCCAGAGATCCTGAAGGAGTTCACCCTGCATGACCACGTGCGGGAG
                                                                              GCAAAAGGAGTCACTTGTTACGTCGCAGGAAGAGCCTTCTGATGGGAA 1068
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HTG; HTGS_PHASE1.
Rattus norvegicus.
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Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Chen, G., Chondhry, I., Christopoulos, C., Chen, G., Chen, G., Chondhry, I., Christopoulos, C., Chen, G., Char, G., Cox, C., Coyle, M.D., Dathornes, S.R., David, R., Davilla, M.L., Davilla, M.L., Davilla, C.D., Dederich, D.A., Douthwalter, M.J., Draper, H., Dugan-Rocha, S., Dubbin, K.J., Barnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraquto, D., Flagg, N., Ford, J., Foster, P., Frantz, P. Garlis, A., Gao, J., Gardia, A., Garner, T., Garza, N., Gill, R., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hennandez, J., Harnandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Harris, K., Hart, M., Havlak, P., Hawes, A., Hollins, B., Jacobson, B., Jia, Y., Johnson, R., Jollins, E., Jackson, E., Kelly, S., Khan, U., King, L., Korvah, J., Garsen, K., Karlovic, J., Kurtovic, J., Kursenh, A., House, M., Mollins, B., Lowis, L., Lu, X., Lucier, A., Louier, R., Luna, R., Martine, E., Massey, E., Mawhiney, E., Martin, R., Morden, M., Molwen, M., Molwen, M., Noken, W., Stake, R., Erims, F., Tang, H., Stake, R., Tang, H., Stoken, R., Stake, R., Palmer, J., Stoken, R., Palmer, S., Sochere, S., Sochere, R., Palmer, S., Sochere, S., Sochere, R., Stake, A., Taneria, A., Tang, H., Tang, H., Sulton, A., Walliams, G., Walli
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Direct Submission
Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Modecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Jul 19, 2002 this sequence version replaced gi:20806241.
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Direct Submission
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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GVVADRGYLEKALDRFRARYSSPVFVVTSNOMANORBYINTSLGDVVFAGNGIBGSPR
KDFALÍTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKIFKPAAFLPEM
MGIPADLSPLLKH"
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MHNALAPIFRISLPVLHSDTARRIPWONYHLNNWMEERYRHIPGOYVRFTGYPCSWTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MASAQVPFSFPLAHFLIFVFVTSTIIHLQQRIVKLQTLSEKELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YHHLRPEILKEFTLRDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPKVWK
                                                                                                                                                                                                                                                                                             /EC_number="2.4.1.69"
/note="fucosyltransferase; similar to the Mus musculus strain ICR Sec2 sequence deposited at GenBank Accession Number AF064792; similar to the Homo sapiens secretor blood group alpha(1,2)fucosyltransferase FUT2 sequences deposited at GenBank Accession Numbers D87942 and U17894"
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/gene="Fut2"
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/protein_id="AAF45146.1"
/db_xref="G1:7288505"
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/cell_line="E14"
/cell_type="ES"
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                                                       /organism="Mus musculus"
/strain="129/Ola"
/db_xref="taxon:10090"
/chromosome="7"
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Domino,S.E., Zhang,L. and Lowe,J.B. Molecular cloning, genomic mapping, and expression of two secretor blood group alpha (1,2)fucosyltransferase genes differentially regulated in mouse uterine epithelium and gastrointestinal tract J. Biol. Chem. 276 (26), 23748-23756 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3. (bases I to 6762)
Domino, S.E. and Lowe, J.B.
Direct Submission
Submitted (13-DEC-1999) HHMI, University of Michigan, 1150 W. Med.
                                                                                                          GGGTGTCCATGTGCGCCGAGGGGACTATGTGCATGTCATGCCTAATGTGTGGAAGGGCGT
                                                                                                                          GGTGGCTGACCGGGGTTACCTGGAAAAGGCCCTGGATATGTTCCGGGCACGCTATTCATC
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Domino,S.E. and Lowe,J.B.
Mus musculus alpha(1,2)fucosyltransferase FUT2 (Sec2) genomic
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RESULT 7

ACCESSION VERSION KEYWORDS SOURCE

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TITLE

REFERENCE AUTHORS JOURNAL

JOURNAL

COMMENT

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Consensus quality: 191947 bases at least 040
Consensus quality: 197212 bases at least 030
Bitimated insert size: 199546; sum-of-contigs estimation
Quality coverage: 7.3 in 020 bases; agarose-fp estimation

* NOTE: This is a 'working draft' sequence. It currently
consists of 14 contigs. Gaps between the contigs
are represented as runs of N The order of the picces

* Somists of 14 contigs. Gaps between the sizes
of the gaps between them are based on estimates that have
provided by the submitter of N The order of the sizes

* This sequence will be replaced

* This sequence will be replaced

* The sequence will be preserved.

* This sequence will be preserved.

* This sequence will be replaced

* This sequence of 16266 bp in length

* 16257 16356; contig of 16256 bp in length

* 1655 38025 38124; gap of unknown length

* 60460 66599; gap of unknown length

* 60560 66982: contig of 4333 bp in length

* 60560 66983: contig of 4333 bp in length

* 11367 111466; gap of unknown length

* 11367 113014: contig of 1848 bp in length

* 113015 113014: gap of unknown length
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f unknown length
g of 4877 bp in length
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contig of 3954 bp in length
gap of unknown length
contig of 1835 bp in length
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Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 18, 2000 this sequence version replaced 9::8810391.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musiae; Mus
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                                                                                          3110 TACCTGGCAGGTGGTACCATCTACCTAGCCAACTACACCTTCCGGATTCTCCGTTC
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Center: Joint Genome Institute
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HTG; HTGS_PHASE2; HTGS_DRAFT
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DOE Joint Genome Institute.
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bp in length

Gaps

us-10-040-863-9.rge

301 GACACGGCCAAAAAAATCCCATGGCAGAA	Qy	ON Mus musculus GDP-L-fucose;beta-D-galactoside 2-alpha-1-fucoswitransferses mbws complete 340
301 GAATCCATGCACACGCTCTAGCGCCCA)	qa	AF064792 LOCUS AF064792 1044 bp mRNA linear ROD 24-00T-2000
241 GCATCCATGCACACGCTCTAGCGCCCA	δŏ	NET 8
241 GGGGAATAGGTACATTGTTTGCACTGG	<u>بر</u> م	Db 12937 GCAGAAGGAGTCACTTGGTACATCCCAGGAGGCCTTCTACTGGGAA 12890
	g 2	1001
121 AATGGAGGTGCGGGGCATGTTCACGA	δ i	99 961 CTGTCCCCACTCCTTAAGGCATTAACACCAGCTGTCCGGGTCCCACTTCCACTCCAAG 1020 DD 12997 CTGTCCCCATTCTTAAGCATTAAAAAAAAAAAAAAAAAA
	qa	Db 13057 CTChararttttargccagcagcagccgtcccccgagtggatgggatg
61 CAAATGTCCTCGGGAAACACAGAAAGCC	δŽ	QY 901 CTCAAAGTCTTTAAGCCAGGGGGCCTTCCTACCGGATGGGTGGG
1 CICCAGCAGCAATAGIGAAGCICCAAC 	da da	13
Query Match Best Local Similarity 89.9%; Pred. No Matches 879; Conservative 0; Mismai	Query Best I Matche	
229 a	BASE COUNT ORIGIN	721
AVOMSSPNAARTDMOGENKLOV MHNALAP IFRISLPVLHSDTAN YHHLRPBILKEPTLHDHVRERE GVVADRGYLEKALDRFRARY S:		OY 661 CCAGTCTTCGTGGTTACAACGATATGGCCTGGTGCCGGGAGAACATTAATGCTTCC 720 DD 13297 CCAGTCTTCGTGGTTACAAGCAAAGGGTTTGCTGCCGGGAGAACATCAACATCC 13238
<pre>2-alpha-1-tucosyltrans /protein_id="AACIG887 /db_xxef="G1:3142706" /translation="MASAQVPI</pre>		QY 601 GIGGCIGACCGGGGTTACCTGGAAAAGGCCCTGGATATGTTCCGGCCACGCTATTCATCT 660 DD 13357 GIGGCIGACCGGGGTTACCTAGAAAAGGCCCTGGACAGGTTCCGGGCACGCTATTCATCT 13298
/EC_number="2.4.1.69" /note="sec2; Se" /codon_start=1 /product="GDP-L-fucoso		Qy 541 GGTGTCCATGTGCGCCGAGGGGACTATGTGCATGCCTAATGTGTGGAAGGCGTG 600
	SOS	481 GAGGCCCAGGCTTCCTGCGGGTCTGCGGGTGAATGGGAGCCGGCGGGTTTTTGTG 540
Kinki University, Kowakae, Hige ES Location/Qualifiers ource 11044 /organism="Mus muscul	FEATURES Sou	421 TACCACCACCAGGCCCACAGATCCTGAAGAGTTCACCCTGCATGACCACGGGGGG 480
	AUTHORS TITLE JOURNAL	9y 351 TACCSCCACAITCCGGGACACTTGTGCGCTTCACGGGATACCCGTGCTCCTGGACCTTC 420 Db 13597 TACCGCCACATCCCGGGGCAGTATGTGCGTTTCACGGGATACCCGTGCTCCTGGACCTTC 13538
L Biochim. Biophys. Acta 1487 (2 ² 20471982 D 11018479 E 2 (bases 1 to 1044)	JOURNAL MEDLINE PUBMED REFERENCE	OY 301 GACACGGCCAAAAGATCCCATGGCAGAATTACCATCTCAACGACTGGATGGA
	TITEE	Qy 241 GCATCCATGCACAACGCTCTAGGGCCCATCTTCAGGATCAGCTCTCCGGGTGTTACACAGC 300 L3717 GAATCCATGCACAACGCTCTAGGGCCCATCTTCAGGATCAGTCTCCCGGTGTTACACAC 13658
Iwamori, M.	_	Db 13777 GGCGAATATGCTACATTGTTTGCACTGGCCAGGATGAACGGTCGGCTTGCCTTCATCCCT 13718

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SWAYLAGGDTIYLANYTLPDSPFLKIFKPAAAFLPEW
                                                                                                                                                        stry, Faculty of Selence & Technology, gashi-osaka 577-8502, Japan
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alphal,2-fucosyltransferase, MFUT-II, duced in a restricted region of the mice by host-microbe interactions and
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7.1"
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14

ARUD4/92 1044 bp mRNA lines Mus musculus GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase mRNA, complete cds. AF064792

AF064792.1 GI:3142705

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

Mus musculus.
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1044)
Lin,B., Hayashi,Y., Saito,M., Sakakibara,Y., Yanagisawa,M. and

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us-10-040-863-9.rge

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/product="GDP-L-fucose:beta-D-galactoside
2-alpha-1-fucosyltransferase"
2-alpha-1-fucosyltransferase"
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HDHVREBAQAFLRGIRNNGSQPSTFVGYHVRRGDYVHVMFKWWRGYVALDRGYLEKALD
RFRARYSSPVFVYTSNGMAWGRENINTSLGDYVFAGNGIEGSPAKDFALLTQCNHTIM
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Pred. No. 2.2e-190;
0; Mismatches 74;
                                                               /Ec_number="2.4.1.69"
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89.9%;
                                               /gene="FUT2"
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/qene="FUT2"
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Liu, Y. and Saitou, N.
Direct Submission
Submitted (19-FEB-2000) Naruya Saitou, National Institute of
Genetics, Laboratory of Evolutionary Genetics; 1111 Yata, Mishima,
Shizuoka 411-8540, Japan (E-mail:nsaitou@genes.nig.ac.jp,
URL:http://sayar.lab.nig.ac.jp/, Tel:81-559-81-6790,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
              CTGCTCACCCAGTGCAACCACACCATCATGACTATTGGGACCTTTGGGATTTGGGCTGCC
                                                                                                                                                                                                                                                                                                                                                                        TACCTGGCAGGTGGTGATACCATCTAGCCAACTACACCCTTCCGGATTCTCCGTTC
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                                                                                                   GIGGCIGACOGGGGTIACCIGGAAAAGGCCCTGGAIAIGTICCGGGCACGCTATTCATCT
                                                                                                                                                                                   GTGGCTGACCGGGGTTACCTAGAAAGGCCCTGGACAGGTTCCGGGCACGCTATTCATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus FUT2 gene for GDP-L-fucose:beta-D-galactoside
2-alpha-1-fucosyltransferase, partial cds, strain:C57BL/10snJ.
AB039114
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Mus musculus
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AUTHORS
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JOURNAL

TITLE

FEATURES

REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS

RESULT 9 AB039114

120 138 180 198 240 258 300 318 360 378 420 438 480 498 540 558 009 618 099

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RFRAFYSSPYFVTSNGMAMCRENINTSLGDVVFAGNGIEGSPAKDFALLTQCNHTIM
TGFFGINAAYLAGGINAAYLLPDSPFLKIFKPAAFLPEWM"
285 2 257 9 207 t
                                                                                                                                                                                                                                                        AB039115
Mus musculus FUT2 gene for GDP-L-fucose:beta-D-galactoside
2-alpha-1-fucosyltransferase, partial cds, strain:BFM/2Msf.
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QQSAKLQGIFTINSIGRLGNQMGEYATLFALARMNGRLAFIPESMHNALAPIPRISLP
                                                                                                                                                                                                                                                                                                                          FUT2; GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase.
Mus musculus (sub_species:brevirostris, strain:BFM/2Msf) DNA.
Mus musculus
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                                                                                                                 Genes
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
CTGCTCACCCAGTGCAACCACCATCATGACTATTGGGACCTTTGGGATTTGGGCTGCC
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-2-alpha-1-fucosyltransferase"
/protein_id="Bab68659.1"
/db_xref="GI:15822976"
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Pred. No. 2.2e-190;
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/db_xref="taxon:10090"
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Acc#AF064792"
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/strain="BFM/2Msf"
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/EC_number="2.4.1.69"
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Liu, Y. and Saitou, N.
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QSAKLQGIPTINSIGRLGWGEVATTEALARMNGRIAFIEPSEMHRAAPIFRISLP
VLASDTARRIFPWQNYRLINDWMBERXTEFRALF
YLLSDTARRIFPWQNYRLINDWMBERXFIFTALFALARMNGRAFIEFSELF
HDHVRDEAQAFLRGRYNGSQPSTFVCVHVRRGDYHHWMFKWKGVYADRGFLEKALD
HDHVRDEAQAFLRGRYNGSQPSTFVCVHVRRGDYHHWMFKWKGVYADRGFLEKALT
RTGREGIWAAYLAGGDIIXLANYTLDSSFELKIFKPAAAFLDFGWM"

1 285 - 27 - 97 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 977 - 9
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                     FUT2; GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase Mus musculus (sub_species:musculus, strain:BLG2/Msf) DNA.
                                                                                                                                                                                                                                                                                                     2. (bases 1 to 963)
Liu,Y. and Saitou,N.
Direct Submission
Submitted (29-FFB-2000) Naruya Saitou, National Institute of
Genetics, Laboratory of Evolutionary Genetics; 1111 Yata, Mishima,
Shizuoka 411-8540, Japan (E-mail:nsaitou@genes.nig.ac.jp,
URL:http://sayer.lab.nig.ac.jp/, Tel:81-559-81-6790,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 AATGGAGAGCTGCGGGGCATGTTCACGATCAATTCCATTGGCCGGCTGGGGAACCAGATG 180
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                                                                                               Eukaryota, Metazoa: Chordata; Craniata; Vertebrata, Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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2-alpha-1-fucosyltransferase"
/protein_id="man68640.1"
/db_xref="GI:15822978"
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Acc#AF064792"
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/db_xref="taxon:10090"
                                                                                                                                                                                                       of Five Mus musculus subspecies
Unpublished
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1. .963
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                                                                          Mus musculus
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Mus musculus FUT2 gene for GDP-L-fucose.beta-D-galactos.de
2-alpha-1-fucosyltransferase, partial cds, strain:CAST/Ei.
AB039117
AB039117. | GI:15822979
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Liu, Y. and Saitou, N.
Liu, Y. and Saitou, N.
Liu, Y. and Saitou, N.
Submitted (29-FEB-2000) Naruya Saitou, National Institute of
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Shizuoka 411-8540, Japan (E-mail:nsaitou@genes.nig.ac.jp,
URL:http://sayer.lab.nig.ac.jp/, Tel:81-559-81-6790,
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                                                                             TACCACCACCTGCGCCCAGAGATCCTGAAGGAGTTCACCCTGCATGACCACGTGCGGGAG
                                                                                                                                                                                GGTGTCCATGTGCGCCGAGGGGACTATGTGCATGTCATGCCTAATGTGTGGAAGGGGCGTG
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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QQSAKLQGIFTINSIGRLGNOMGEYATLFÄLARÄNGRLAFIPESMHNALAPIFRISLP
VLHSDTARRIPWQNYHLNDWMEERYRHIPGQYVRFTGYPCSWTFYHHLRPEILKEFTL
HDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDXVHVMPKVWKGVVADRGYLEKALD
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Mus musculus (sub_species:molossinus, strain:MSM/Msf) DNA.
Mus musculus
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Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes
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Direct Submission
Submitted (29-FEB-2000) Naruya Saitou, National Institute of Genetics, Laboratory of Evolutionary Genetics; 1111 Yata, Mishima, Shizuka 411-8540, Japan (E-mail:nsaitou@genes.nig.ac.jp, URL:http://sayer.lab.nig.ac.jp/, Tel:81-559-81-6790,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
619 GIGGCTGACCGGGGTTACCTAGAAAGGCCCTGGACAGGTTCCGGGCACGCTATTCATCT
                                         CCAGTCTTCGTGGTTACAAGCAACGGTATGGCCTGGTGCCGGGAGAACATTAATGCTTCC
                                                             CIAGGAGACGIGGIGITIGCGGGCAATGGIATTGAGGGCTCACCAGCCAAGGACTTCGCG
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                                                                                                                           CGAGGAGACGTGGTTCGCGGGCAATGGTATTGAGGGGTCGCCAGGCAAGGACTTCGCG
                                                                                                                                                                                                             CTGCTCACCCAGTGCAACCACACATCATGACTATTGGGACCTTTGGGATTTGGGCTGCC
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Mus musculus FUT2 gene for GDP-L-fucose:beta-D-galactoside
2-alpha-1-fucosyltransferase, partial cds, strain:MSM/Msf.
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2-alpha-1-fucosyltransferase"
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/db_xref="taxon:10090"
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/db_xref="GI:15822982"
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/EC_number="2.4.1.69"
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AB039118.1 GI:15822981
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QQSAKLQGIFIINSIGRLGNQMGEYATLFALARMNGRLAFIPESMHNALAPIFRISLP
VLHSDTARRIPWQNYHLNDWMEERYRHIPGQYVRFTGYPCSWTFYHLRPEIIKEFTL
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RPRAKSSRPYVYTGNGMAMCRENINTSLGDVVFAGNGIEGSPAKDFALLTQCNHTIM
TIGTPGIWAAYLAGGDTAAYTLADYTLPDSPFLKTFKPAAAFLPEWM"
285 c 257 g 207 c
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                                                                                                     /note="sequence used for primer design based Acc*AF064792"
                                                                                                                                                                                                                                                                                        /product="GDP-L-fucose:beta-D-galactoside
-2-alpha-1-fucosyltransferase"
/protein.id="RBB68641.1"
/db_xref="G1:15822980"
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89.9%; Pred. No. 2.2e-190;
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'organism="Mus musculus"
                                         /sub_species="castaneus"
                                                             /db_xref="taxon:10090"
                                                                                                                                                                                                      /gene="FUT2"
/BC_number="2.4.1.69"
/note="Sec2; Se"
                   /strain="CAST/Ei"
                                                                               /chromosome="7
                                                                                                                                                                                                                                                                         /codon_start=1
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      TIGTECIWAAYLAGGDTIYLANYTLƏDSPFLKIFKPAAAFLPEWM
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                                                  Score 764.6; DB 10;
Pred. No. 2.2e-190;
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                                                   71.68;
89.9%;
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FERARXSSPYVVYISNGMAWCRENIWTSLGDVVFAGNGIEGSPAKDFALLTQCNHTIM
TIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKIFKPAAAFLPEWM"
1 285 C 17 G 207 L
AB039119
Mus musculus FUT2 gene for GDP-L-fucose:beta-D-galactoside
2-alpha-1-fucosyltransferase, partial cds, strain:pgn2.
AB039119.1 GI:15822983
FUT2: GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase.
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QQSAKLQGIFTINSIGRLGNQMGEYATLFALARMNGRLAFIPESMHNALAPIFRISLP
VLHSDTARRIPWQNYHLNDWMEERYRHIPGQYVRFIGYPCSWTFYHHLRPEILKEFTL
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Liu,Y. and Saitou,N.
Direct Submission
Submitsed (29-FEB-2000) Naruya Saitou, National Institute of
Genetics, Laboratory of Evolutionary Genetics; 1111 Yata, Mishima,
Shizuoka 411-8540, Japan (E-mail:nsaitou@genes.nig.ac.jp,
URL:http://sayer.lab.nig.ac.jp/, Tel:81-559-81-6790,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                  Mus musculus (sub_species:domesticus, strain:pgn2) DNA
                                                                                                                                                                                                                                                                                              Liu,Y., Kitano,T., Koide,T., Shiroishi,T., Moriwaki,K. Saitou,N.
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="pgn2
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/gene="FUT2"
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GCATCCATGCACAACGCTCTAGCGCCCATCTTCAGGATCAGCCTCCCGGTGTTACACAGC
                                                                                          TACCGCCACATTCCGGGACACTTTGTGCGCTTCACGGGATACCCGTGCTCCTGGACCTTC
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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of Five Mus musculus subspecies

Unpublished

DEFINITION

RESULT 15 AB039120 LOCUS

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ACCESSION

VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS 2 (bases 1 to 963) Liu,Y. and Saitou,N. Direct Submission

AUTHORS

REFERENCE

JOURNAL

TITLE

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QGSAKLQGIFTINSIGRLGNOMGEYATLFÄLARMNGRLAFIPESMHNALAPIFRISLP
VLHSDTARRIPWQNYHLNDWMEERYRHIPGQYVRFTGYPCSWTFYHHLRPEILKEFTL
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1 285 c 257 g 207 t
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Submitted (29-FEB-2000) Naruya Saitou, National Institute Genetics, Laboratory of Evolutionary Genetics: 1111 Yata, Shizuoka 411-8540, Japan (E-mail:nsaitou@genes.nig.ac.jp, GRL:http://sayer.lab.nig.ac.jp/, Tel:81-559-81-6790, Fax:81-559-81-6799)
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89.9%; Pred. No. 2.2e-190;
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Search completed: May 26, 2003, 14:49:17 Job time : 2883.28 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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                                                                 The present sequence is given in a specification relating to a rat ganglisciate Specific alphal-Ziucosyltransferase protein. The protein or its cellular fraction is useful for synthesis of a molecule comprising Pucalphal-ZGalbetal-3GalNac, a glycolipid, glycoprotein, glycolipoprotein or a free oligosaccharide comprising Fucalphal-ZGalbetal-3GalNac. The method involves contacting alphal-Ziucosyltransferase with GDP-fucose and a molecule or glycolipid, glycoprotein, glycolipoprotein or useful for synthesis of fucesyl-GML by contacting the protein with GDP-fucose and ganglioside GML1. The obtained glycoproteins,
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rat ganglioside GMI-specific alphal-2Fucosyltransferase, useful for paration of fucosyl GMI which is useful as a nutritional composition immunotherapeutic for cancer and neurological diseases -
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                                                                                                                                                                                glycolipoproteins, glycolipids and oligosaccharides are useful as nutritional compositions and fucosyl-GM_I is useful for inducing a immunotherapeutic or immunosuppressive action against cancer, neurological disease or small cell lung carcinoma.
                                                                                                                                                                                                                                                               100.0%; Score 1068; DB 21; Length 1068; 100.0%; Pred. No. 8.5e-289; ive 0; Mismatches 0; Indels 0;
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                                              Fig 3A; 91pp; English
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GMI-specific alphal-2fucosyltransferase enzyme by recombinant
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(alphal-2Fuct) enzyme and its corresponding nucleic acid. This nucleic acid is specific for a carbohydrate moiety found in ganglioside GM1, a terminal galactose betal-3N-acetylgalactosamine (Galbetal-3GalNac) saccharide. Alphal-2FucT DNA is useful for producing rat alphal-2FucT protein by recombinant techniques. Alphal-2FucT DNA is useful for the proparative synthesis of fucosyl containing glycolipids, glycolipids, glycolipids, glycolipids, glycolipids as a seguine and oligosaccharide, and for preparing fucosyl-GM1. Alphal-2FucT DNA is useful for detecting oncogenic transformation which involves assaying for changes in expression of alphal-2FucT sactivated in cell transformation, antisense sequences derived from alphal-2FucT DNA are useful for inhibiting, suppressing antisense therapy. The present sequence is rat hepatoma H35 cell alphal-2FucT catalytic domain encoding DNA.
  techniques and for detecting oncogenic transformation of test tissues
                                                                                                           invention relates to rat GMI-specific alphal-2fucosyltransferase
                                                        41pp; English
                                                        Fig 3;
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Sequence 1068 BF; 237 A; 308 C; 300 G; 223 T; 0 other;

Query Match Best Local Similarity	100.0%;	100.0%; Score 1068; DB 24; Length 1068; 100.0%; Pred. No. 8.6e-289;	В 24; :-289;	Length	1068;		
Matches 1068; Conservative U; Mismatches U; Lindels U; Gaps	vative U;	be; Conservative U; Mismatches U; Indels U; Gaps (Indels	0;	Gaps	.; o

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961 CIGTCCCCACTCCTIAAGGCAITAACACCGGCCTGICCTCGGICCCACTTCCACCTCAAG 1020 780 840 006 096 006 CTGTCCCCACTCCTTAAGGCATTAACACCAGCCTGTCCTCGGTCCCACTTCCACCTCAAG 841 IACCTGCCAGGTGGTGATACCATCTACTTAGCCAACTACACCGTTCCGGATTCTCCGGTTC CTGCTCACCCAGTGCAACCACACCATCATGACTATTGGGACCTTTGGGÄTTTGGGCTGCC TACCTGGCAGGTGGTGATACCATCTACTTAGCCAACTACACCCTTCCGGATTCTCCGTTC GCAAAAGGAGTCACTTGTTACGTCGCAGGAAGAGCCTTCTGATGGGAA 1068 841 1021 781 721 721 781 901 901 961 g g a ŏ qq ŏ g $^{\circ}$ ŏ g á

ВР AAC67965 standard; cDNA; 1149 (first entry) 19-FEB-2001 RESULT 3 AAC67965

Rat; alphal-2fucosyltransferase; cytostatic; neuroprotective; nootropic; gene therapy; Fucalphal-2Galbetal-3GalNAc; immunotherapy; immunosuppression; cancer; neurological disease; small cell lung carcinoma; ss. Rat hepatoma H35 cell alphal-2fucosyltransferase cDNA

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Rattus norvegicus. WO200064464-A1.

02-NOV-2000

99WO-US07384 99WO-US07384 23-APR-1999; 23-APR-1999;

(PACI-) PACIFIC NORTHWEST CANCER FOUND.

Sherwood AL; WPI; 2000-687262/67. Holmes EH,

P-PSDB; AAB36104

New rat ganglioside GMI-specific alphal-2Fucosyltransferase, useful for preparation of fucosyl GM1 which is useful as a nutritional composition or immunotherapeutic for cancer and neurological diseases

Claim 10; Fig 5; 91pp; English.

009 900 999 099

The present sequence is given in a specification relating to a rat ganglioside GM_1-specific alphal-2fucosyltransferase protein. The protein or its callular fraction is useful for synthesis of a molecule comprising Fucalphal-2Galbetal-3GalNac, a glycolphid, glycoprotein, glycolphoprotein or a free oligosaccharide comprising Fucalphal-2Galbetal-3GalNac. The method involves contacting alphal-2fucosyltrabgierase with GDP-fucose and a molecule or glycolpid, glycoprotein, glycolpoprotein or oligosaccharide having a terminal Galbetal-3GalNac group. It is also useful for synthesis of fucosyl-GM_l by contacting the protein with

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GDP-fucose and ganglioside GM_1. The obtained glycoproteins, glycolipoproteins, qlycolipids and oligosaccharides are useful as nutritional compositions and fucosyl-GM_1 is useful for inducing an immunotherapeutic or immunosuppressive action against cancer, neurological disease or small cell lung carcinoma.
                                                                         3; DB 21; Length 1149;
8.9e-289;
                                                                                            Indels
                                                        Sequence 1149 BP; 247 A; 341 C; 311 G; 250 T; 0 other;
                                                                                  Pred. No. 8.9
0; Mismatches
                                                                         100.0%; Score 1068;
                                                                                  100.08;
                                                                                 Best Local Similarity 100.
Matches 1068; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat hepatoma H35 cell alphal-2fucosyltransferase, useful for producing GM1-specific alphal-2fucosyltransferase enzyme by recombinant techniques and for detecting oncogenic transformation of test tissues
   1042 CTGTCCCCACTCCTTAAGGCATTAACACCAGCCTGTCCTCGGTCCCACTTCCACCTCAAG
                                                                           CIGTCCCCACTCCTTAAGGCATTAACACCAGCCTGTCCTCGGTCCCACTTCCACCTCAAG
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r (Se) glycosyltransferase (see AAM37855), an enzyme ffinity for type I and type III substrates. It was pige I was probe.

If inity for type I and type III substrates. It was probe.

Introduction of glycosyltransferase undman Fyri. Introduction of glycosyltransferase undman Fyri. Introduction of glycosyltransferase unch as porcine Se nucleic actio, into a tissue ced expression of unwanted carbohydrate epitopes on estable for transplantation, i.e. less for increased immunological acceptability. A lof increased immunological acceptability. A cacceptable to a recipient species involves reducing hydrate on the donor cell that causes it to be non-self by the recipient pecies involves reducing hydrate on the donor cell that causes it to be non-self by the recipient by causing a nucleic acid ransferase such as Se to be expressed in the cells. S, such as retroviral packaging or producer cells, nucleic acids can be used in gene therapy.
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                                                                                     TCACTTGTTACGTCGCAGGAAGAGCCTTCTGATGGGAA 1068
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Pig; secretor; chimeric; glycosyltransferase; gene therapy;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes pig secretor used in an example of the present invention describes nucleic acids (NA) encoding a chimaric glycosyltransferase. The NAs comprise a catalytic domain of a first glycosyltransferase (GT) and a localisation signal of a second GT, whereby when the NA is expressed in a cell and where the chimaric enzyme is located in a marea of the cell where it is able to compete for substrate with a second GT, resulting in reduced levels of a product from the second GT. The NAs can be used to produce cells and organs with desired glycosylation patterns. Products and methods of the epitopes in cells, tissues or organs which may be used in needinable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TICAGGATCAGCCTCCCGGTGTTACACAGCGACACGGCCAAAAAAATCCCATGGCAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATTCCATTGGCCGGCTGGGGAACCAGATGGGCGAATACGCCACACTCTTTGCACTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211 AGGATGAACGGACGGCTTGCGTTCATCCCCGCATCCATGCACACGCTCTAGCGCCCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TACCATCTCAACGACTGGATGGAGGGGTTACCGCCACATTCCGGGGACACTTTGTGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TICACGGGATACCCGTGCTCCTGGACCTTCTACCACCACCTGCGCCCCAGAGATCCTGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIGACGCAGGCCACAGAGAGCCCCTCGAGCCCCCAGCTGAAGGGCATGTGGACGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding chimeric glycosyltransferases - used for altering carbohydrate levels on the surface of cells, useful in gene therapy and transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 19; Length 1043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1043 BP; 189 A; 352 C; 306 G; 196 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 612.8; DB 19;
Pred. No. 2.3e-161;
0; Mismatches 172;
                                                                   "secretor'
Location/Qualiflers 9..1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transplantation or gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Fig 6; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.4%;
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nes 716; Conservative
                                                                                                                                                                                                                                                                                                                          (AUST-) AUSTIN RES INST
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                                                                                                                                                                                                             01-AUG-1997;
                                                                                                                                                                                                                                                         21-AUG-1996;
                                                                                                                 WO9805768-A1
                                                                                                                                                                                                                                                                               02-AUG-1996;
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128 AGCTGCGGGGCATGTTCACGATCAATTCCATTGGCCGGCTGGGGAACCAGATGGGCGAAT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence encodes the human Sec2 protein of the invention. The DNA encodes a alpha(1.2) fucosyltransferase and is the Secretor alpha(1.2) fucosyltransferase locus, that cross hybridises with the Hi blood group alpha(1.2) fucosyltransferase gene. The DNA is useful for producing a recombinant human GDP-L-fucose.Deta-D-galactoside 2-alpha-L-fucosyltransferase (FUT2) which can be used for genotyping an individual as a secretor or nonsecretor as it is known that nonsecretors homozygous for a mutant allele of the FUT2 gene that has a stop codon in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              548 ATGTGCGCCGAGGGGACTATGTGCATGTCATGCCTAATGTGTGGAAGGGCGTGGTGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCGTGGTTACAAGCAACGGTATGGCCTGGTGCCGGGAGAACATTAATGCTTCCCGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        728 ACGIGGIGITUCGCGGCCAAIGGIATIGAGGGICGCCAGCCAAGGACTICGCGCIGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 ACGCCACACTCTTTGCACTGGCCAGGATGAACGGACGGCTTGCGTTCATCCCCGCATCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       539 ACCTCCGCCAGGAGATCCTCCAGGAGTTCACCCTGCACGACCACGTGCGGGAGGAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            608 ACCGGGGTTACCTGGAAAAGGCCCTGGATATGTTCCGGGCACGCTATTCATCTCCAGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGTGGTGTTTGCTGGCGATGGCCATTGAGGGCTCACCTGCCAAAGATTTTGCTCTACTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCAGTGCAACCACATCATGACTATTGGGACCTTTGGGATTTGGGCTGCCTACCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248 TGCACAACGCTCTAGCGCCCATCTTCAGGATCAGCCTCCCGGTGTTACACAGCGACAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                             368 ACATTCCGGGACACTTTGTGCGCTTCACGGGATACCCGTGCTCCTGGACCTTCTACCACC
                                                                              recombinant enzyme and genotyping person as secretor or nonsecretor
                                                                                                                                                                                                                                                                                                                                                     55.3%; Score 590.6; DB 19; Length 2115; 79.8%; Pred. No. 5e-155;
                                                                useful for producing
                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                     Sequence 2115 BP; 505 A; 606 C; 552 G; 452 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 179;
                                                                                                                                                                                                                                                                                     the position corresponding to amino acid 143.
                                                                encoding fucosyltransferase enzyme
                                                                                                                  55pp; English
                                                                                                                                                                                                                                                                                                                                                         Query Match 55.3
Best Local Similarity 79.8
Matches 709; Conservative
                                                                                                                Claim 1; Column 45-50;
              WPI; 1998-520127/44.
                                P-PSDB; AAW69332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCTGGTGTCGGGAAAACATCAATGCCTCGCGCGCGATGTGGTGTTTGCCGGCAATGGC
                                                                                                                                                                                                                                                                                                                                                           ATTGAGGGGTCGCCAGCCAAGGACTTCGCGCTGCTCACCCAGTGCAACCACACCATCATG
                                                                                                                                                                                                                                                                                                                                                                              ACTATTGGGACCTTTGGGATTTGGGCTGCCTACCTGGCAGGTGGTGATACCATCTACTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCAACTACACCCCTTCCGGATTCTCCGTTCCTCAAAGTCTTTAAGCCAGAGGCAGCCTTC
                                                                                                                GTGAACGGGAGCCGACCAGTACCTACGTGGGGGTGCACGTGCGCGGGGGGGACTACGTG
                                                                                                                                                    CATGTCATGCCTAATGTGTGGAAGGGCGTGGGTGACCGGGGGTTACCTGGAAAAGGCC
                                                                                                                                                                                      CACGEGAEGCCCAACGEGEGAAGGGCGEGGEGTGGCCGACCGGCGGTACCTGGAGCAGGCC
                                                                                                                                                                                                                      GCCTGGTGCCGGGAGAACATTAATGCTTCCCGAGGAGACGTGGTGTTCGCGGGCAATGGT
                GAGTTCACCCTGCATGACCACGTGCGGGAGGACCCCAGGCCTTCCTGCGTGGTCTGCGG
                                                                                  GTGAATGGGAGCCAGCCGAGTACTTTTGTGGGTGTCCATGTGCGCCGAGGGGACTATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTACCCGAATGGGTGGGCATCCCTGCCGATCTGTCCCCCACTCCTTAAG 978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
64..1095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA; 2115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95US-0395800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sec2 coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GIORGI D.
KELLY R J.
LENNON G.
LOWE J B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV58323 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-1995;
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(LENN/)
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298 247

Gaps

367 478 427

307

547

658 607

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548 ATGIGGCCGAGGGGCTATGIGCATGICATGCCTAATGIGTGGAAGGCGTGGTGGCTG 607
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Best Local Similarity 78.78
Matches 704, Conservative
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                              Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
  CAGGIGGIGGIGATACCAICTAGCCAACTACACCCCTICCGGATICTCCGTTCCTCAAAG
                                                                                                         CCTTACTCAA-GCACTAATGCTGGCCCGTCCTTTGAGACCTTTTCTCCT 1126
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Gaps 0;

DB 24; Length 3088; Indels

Pred. No. 1.2e-154; 0; Mismatches 191;

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406 307 466 367 526 427 547

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The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in comprises a sequence (S) selected from 847 sequences (S) where (I) comprises a sequence (S) selected from 847 sequences (given in ABLG1664 to ABL70110), or is at least 95% identical to (S), where a change in capsession is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a crivity and can properties of the agent. MI can be used in the structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oseoplaqual, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating ductal cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour.
                                                                                                                                                                                                                                                                                                                               Horrigan S;
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2000US-237606P.
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Weaver Z;
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stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineophastic; Wilm's tumour; adenocarcinoma;
                                                   TOGIGGITACAAGCAACGGIATGGCCTGGTGCCGGGAGAACAITAAIGCITCCCGAGGAG 727
707 AIGITOGCCGAGGGGACTAIGICCATGTCATGCCAAAAGTGTGGGAAGGGGGTGGTGGCCG 766
                  ACCEGEGITACCTEGAAAAGGCCCTGGATATGTTCCGGGCACGCTATTCATCTCCAGTCT 667
                                                              ACGIGGIGITCGCGGGCAATGGIATTGAGGGGTCGCCAGCCAAGGACITCGCGCTGCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oesophageal, ovarian, kidhey, prostate or pancreatic cancer,
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27 - SEP - 2000; 2000US - 235863P - 28 - SEP - 2000; 2000US - 235863P - 28 - SEP - 2000; 2000US - 236028P - 28 - SEP - 2000; 2000US - 236034P - 28 - SEP - 2000; 2000US - 236034P - 28 - SEP - 2000; 2000US - 236109P - 29 - SEP - 2000; 2000US - 23611P - 29 - SEP - 2000; 2000US - 236842P - 20 - CCT - 2000; 2000US - 236841P - 02 - CCT - 2000; 2000US - 237178P - 02 - CCT - 2000; 2000US - 23728P - 02 - CCT - 2000; 2000US - 237316P - 03 - CCT - 2000; 2000US - 237316P - 03 - CCT - 2000; 2000US - 237316P - 03 - CCT - 2000; 2000US - 237316P - 03 - CCT - 2000; 2000US - 237316P - 03 - CCT - 2000; 2000US - 237316P - 03 - CCT - 2000; 2000US - 237506P - 03 - CCT - 2000; 2000US - 237506P - 03 - CCT - 2000; 2000US - 237506P - 01 - NOV - 2000; 2000US - 237506P - 01 - NOV - 2000; 2000US - 244867P - 01 - NOV - 2000; 2000US - 244867P - 01 - NOV - 2000; 2000US - 245084P - 01 - NOV - 2000; 2000US - 245084P - 01 - NOV - 2000; 2000US - 245084P - 01 - NOV - 2000; 2000US - 245084P - 01 - NOV - 2000; 2000US - 245084P - 01 - NOV - 2000; 2000US - 245084P - 01 - NOV - 2000; 2000US - 245084P - 01 - NOV - 2000; 2000US - 245084P - 01 - NOV - 2000; 2000US - 245084P - 01 - NOV - 2000; 2000US - 245084P - 01 - NOV - 2000; 2000US - 245084P - 01 - NOV - 2000; 2000US - 245084P - 01 - NOV - 2000; 2000US - 245084P - 01 - NOV - 2000; 2000US - 245084P - 01 - NOV - 2000; 2000US - 245084P - 01 - NOV - 2000; 2000US - 245084P - 01 - NOV - 2000; 2000US - 245084P - 01 - NOV - 2000; 2000US - 245084P - 01 - NOV - 2000; 2000US - 24608P - 01 - NOV - 2000; 2000US - 24608P - 01 - NOV - 2000; 2000US - 24608P - 01 - NOV - 2000; 2000US - 24608P - 01 - NOV - 2000; 2000US - 24608P - 01 - NOV - 2000; 2000US - 24608P - 01 - NOV - 2000; 2000US - 24608P - 01 - NOV - 2000; 2000US - 24608P - 01 - NOV - 2000; 2000US - 24608P - 01 - NOV - 2000; 2000US - 24608P - 01 - NOV - 2000; 2000US - 24600 - 2000 - 24608P - 01 - NOV - 2000; 2000US - 24608P - 01 - NOV - 2000; 2000US - 24608P - 01 - NOV - 2000; 2000US - 24608P - 01 - NOV - 2000 - 24608P - 01 - NOV - 2000 - 24608P - 01 - NOV - 20
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stomach; lung; prostate; panoreas; carcinôma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
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The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABLG164 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or paroreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal car infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour.
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               Score 589.4; DB 24; Length 3088; Pred. No. 1.2e-154; 0; Mismatches 191; Indels 0;
723 A; 839 C; 798 G; 728 T; 0 other;
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GGCATGTTCACGATCAATTCCATTGGCCGGCTGGGGAACCAGATGGGCGAATACGCCACA 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             354
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                                                  transferase; chimeric; glycosyltransferase; gene therapy;
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Pred. No. 1.9e-108;
0: Mismatches 252; Indels 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1098 BP; 181 A; 367 C; 312 G; 238 T; 0 other;
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Pig H transferase encoding cDNA
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AAV21640 standard; cDNA; 1098

RESULT 11

AAV21640

AAV21640 ID AAV2 XX AC AAV2

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                                                                                                                                                                               to E coli infection.
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                                                                                                                                                                                                                                                                                                                  GAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGG
                CCAGAGATCCTGAAGGAGTTCACCCTGCATGACCACGTGCGGGAGGAGGCCCAGGCCTTC
                                                              CAGTGCAACCACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCT
                                                                                                                                                                                                                                                                              GAGCAGATCCGCAGCGAGTTCACCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGGTA
                                                                                       GTGCGCCGAGGGGACTATGTGCATGTCATGCCTAATGTGTGGAAGGGCGTGGTGGCTGAC
                                                                                                        GTGCGCCGCGGGGACTATCTGCGTGTGATGCCCCAAGCGCTGGAAGGGGGTGGTGGTGAC
                                                                                                                          CGGGGTTACCTGGAAAAGGCCCTGGATATGTTCCGGGCACGCTATTCATCTCCAGTCTTC
                                                                                                                                           GGCGCTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGGATACGAAGCCCCCGTCTTT
                                                                                                                                                             GTGGTTACAAGCAACGGTATGGCCTGGTGCCGGGAGAACATTAATGCTTCCCGAGGAGAC
                                                                                                                                                                                                CAGTGCAACCACCATCATGACTATTGGGACCTTTGGGATTTGGGCTGCCTACCTGGCA
                                                                                                                                                                                                                                                                     GGTGGTGATACCATCTACTTAGCCAACTACACCTTCCGGATTCTCCGGTTCCTCAAAGTC
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                                                   CTGCGT-----GGTCTGCGGGTGAATGGGAGCCAGCCGAGTACTTTGTGGGGTGTCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fragment of pHT83xF encoding swine alpha(1,2) fucosyltransferase
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                                                                                                                                                                The present sequence encodes swine alpha(1,2) fucosyltransferase (FUII). The specification describes methods relating to Escherichia coli-resistant swine. One of the methods for identifying a swine resistant to E. coli-associated intestinal disorders, comprises determining whether the base at 307 of alpha(1,2) fucosyltransferasel gene (FUII) is adenine (sic), in which case the swine are resistant. I porcine FUII polymorphisms can be used to develop drugs for the treatment of swine having E. coli-associated disease. The methods can also be used in breeding programmes to identify swine with resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 GGGACCTGGACTATTACCGGGATGGCGGTTGGGAACCAGATGGGAACGTATGCCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
Identifying swine genetically resistant to E. coli associated diseases - using PCR-RFLP to assay for polymorphisms in the alpha(1,2) fucosyltransferase 1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1269 BP; 219 A; 413 C; 362 G; 275 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 423.8; DB 20;
Pred. No. 2e-108;
); Mismatches 252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ·;
                                                                                                             Claim 6; Fig 1; 19pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.78;
69.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Gaps

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362 315

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and the assay itself is used as a basis for a kit, applied to swine of any age, in detecting polymorphisms associated with E. coli F18 receptors. The polymorphisms are useful in developing drugs to treat swine with E. coli-related diseases. However, a mutated form of the porchine FUTI gene may interfere with the normal enzyme and prevent it from producing the intestinal receptor for F18. The detection of polymorphic markers in the method disclosed enables the detection and treatment of E. coli-related intestinal diseases in swine, where there
                                                                                                                                                                                                                                                                                                                  543 GAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - CTGCTGGCCCTGGCGCAGCCTGCAGGCCTTCATCCAGCCTGCCATGCAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTCTAGCGCCCCATCTTCAGGATCAGCCTCCCGGTGTTACACAGGGGACACGGCCAAAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  603 CIGAGICAGIICCGICIACCCCGCACAGGGGACCGCCCAGCACCIICGIGGGGGICCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        610 CGGGGTTACCTGGAAAAGGCCCTGGATATGTTCCGGGCACGCTATTCATCTCCAGTCTTC
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                                                                                                                                                    has been no success using antibiotics due to unsuccessful prophylaxis
                                                                                                                                                                                                                                                                                              136 GCCATGTTCACGATCAATTCCATTGGCCGGCTGGGGAACCAGATGGGCGAATACGCCACA
                                                                                                                                                                                                                                                                                                                                                                    CTCTTTGCACTGGCCAGGATGAACGGACGGCTTGCGTTCATCCCCGCATCCATGCACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               423 GCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGCCGAGGATTATGCCCACTTAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGACACTTTGTGCGCTTCACGGGATACCCGTGCTCCTGGACCTTCTACCACCACCTGCGC
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                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                            252; Indels
                                                                                                                                                                                      Sequence 1269 BP; 219 A; 413 C; 362 G; 275 T; 0 other;
                                                                                                                                                                                                                           DB 20;
                                                                                                                                                                                                                         Score 423.8; DB Pred. No. 2e-108;

 Mismatches

                                                                                                                                                                                                                       39.78;
69.68;
                                                                                                                                                                                                                                                          Matches 591; Conservative
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                                                                                                                                               1023 TTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCA 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A method has been developed for the identification of swine that are resistant to intestinal colonisation by E. coli. The method comprises determining whether a genetic polymorphism associated with resistance to colonisation is present in a swine sample, and then inferring that the swine is resistant if it is homozygous for the polymorphism. The method uses the swine alpha-1.2-fucosyltransferase (FUT1) polymorphism. The present sequence encodes swine FUT1. The method enables the breading of swine that are resistant to E. coli-related diseases. This method comprises breeding swine that have a genetic polymorphism in the FUT1 are resistant to E. coli-related intestinal disorders if, in a sample taken, the only nitrogen base at residue 307 in the FUT1 gene is adenine. Larger amplified fragments from the assay can be used for FFLP analysis,
                                                           606
                                                                                                                                  969
GGTGGTGATACCATCTACTTAGCCAACTACACCCTTCCGGATTCTCCGTTCCTCAAAGTC
                                                                                           GGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCCACTTCCAGCTTCCTGAAGATC
                                                                                                                            TITAAGCCAGAGGCATTCCTACCCGAATGGGTGGGCATCCCTGCCGATCTGTCCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New method of identifying swine that are resistant to intestinal colonisation by Escherichia coli - comprises use of genetic polymorphic markers, used for breeding swine resistant to Escherichia coli-related diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Swine, pig, alpha-1,2-fucosyltransferase 1; FUT1; resistance; Escherichia coli; infection; oedema; postweaning diarrhoea; intestinal disorder; polymorphism; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                Swine alpha-1,2-fucosyltransferase 1 encoding DNA
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                                                                                                                                                                                                                                                                                                                             BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Swine; pig;
Escherichia
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GGCATGTTCACGATCAATTCCATTGGCCGGCTGGGGAACCAGATGGGCGAATACGCCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is the nucleotide sequence of the pig FUTI gene encoding alpha1-2 fucosyltransferase (see AAY9302). A polymorphism at position 307 of the coding region is associated with susceptibility to F18 Escherichia coli colonization; pigs homozygous for adenine at position 307 are resistant to colonization, while heterozygous animals homozygous for quanime at position 307 are resistant to colonization. A claimed method for improving weight castant to E. coli colonization and feeding these animals high levels of plant-based protein concentrate. A claimed method for preventing F18 E coli colonization in swine, especially swine that are genetically susceptible to F18 E. coli colonization in swine, especially swine that are genetically susceptible to F18 E. coli colonization in swine, replacing some or all of the plant-based proteins in the diet with unimal-based proteins. The polymorphism in the FUTI gene is also associated disease. The polymorphism in the FUTI gene is also per-RFLP tests (see also AAZ9418-19).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Improving weight gain in swine using swine genetically resistant
Escherichia coli and feeding swine high levels of plant based protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.7%; Score 423.8; DB 21; Length 1269; 69.6%; Pred. No. 2e-108; ative 0; Mismatches 252; Indels 6;
                                                                                                                                                                                                                                                                                                          /*tag= 'b
/note= "adenine is substituted for guanine
resistant pigs"
                                                                                                                                                                                                                                                                     /*tag= a
/transl_except= (pos:726..728, aa:Ala)
replace(315,A)
                                                                                                                                                                               FUT1; pig; polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1269 BP; 219 A; 413 C; 362 G; 275 T; 0 other;
                                                                                                                                                     Pig alpha-1-2 fucosyltransferase FUT1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                BIOTECHNOLOGY RES & DEV CORP. US SEC OF AGRIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
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                                                                            ВР
                                                                                                                                                                             Alpha-1-2 fucosyltransferase;
Escherichia coli; resistance;
                                                                           AAZ94417 standard; DNA; 1269
                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0151592
                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US21408
                                                                                                                            (first entry)
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Best Local Similarity 69.6
Matches 591; Conservative
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1083 CTCCAGATG 1091
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                                                                                                                                                                                                                                                                                                                                                             WC200016641-A1
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                                                                                                                            18-JUL-2000
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                                                                                                                                                                                                                     Sus scrofa
                                                                                                                                                                                                                                                                                               variation
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(USDA)
                                                            AAZ94417
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Gaps

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495
243 GGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACG 302
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                                                                                                               GCTCTAGCGCCCATCTTCAGGATCAGCCTCCCGGTGTTACACAGGGACACGGCCAAAAAG 315
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                                                               GTCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCAC
                                                                                                                                                                               316 ATCCCATGGCAGAATTACCATCTCAACGACTGGATGGAGGAGCGTTACCGCCACATTCCG
                                                                                                                                                                                                  423 GCTCCTTGGCGGGAGCTGGAGCTTCACGACGATGTCCGAGGATTATGCCCACTTAAAG
                                                                                                                                                                                                                                                GGACACTTTGTGCGCTTCACGGGATACCCGTGCTCCTGGACCTTCTACCACCTGCGC
                                                                                                                                                                                                                                                                       483 GAGCCCTGGCTGAAGCTCACCGGCTTCCTCGGACCTTCTTCCACCACCACCGCGG
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(BIOT-) BIOTECHNOLOGY RES & DEV CORP (USDA ) US SEC OF AGRIC.
                                                                                     Bosworth B, Ridpath J,
Escherichia coli;
                                                                                            WPI; 2002-391652/42.
P-PSDB; AAB47995.
                                                           18-SEP-1998;
                                                                   20-MAY-1997;
                                            US6355859-B1
                                                    12-MAR-2002
       scrofa
                              mutation
F18;
        Sus
              Key
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97US-047181P 98US-0151592

m,

Feeding swine genetically susceptible to F18 Escherichia coli colonization with a low plant protein based diet increases weight gain and lowers intestinal disease associated with E. coli infection This sequence represents the swine alpha (1,2) fucosyltransferase (FUT1) gene. A FUT1 gene in which there is a base other than adenine at position 307, may be used for improving weight gain in swine that are genetically susceptible to F18 Escherichia coli. The weight gain may be activated by feeding a diet of at least 40% animal based proteins. The feeding method is used to control F18 E. coli associated intestinal disease in swine. Sequence 1269 BP; 219 A; 414 C; 361 G; 275 T; 0 other; Claim 1; Column 13-18; 9pp; English.

completed: May 26, 2003, 12:08:26

Job time

Search

195 315 GGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACG 302 255 362 422 375 482 435 CTGCGT-----GGTCTGCGGGTGAATGGGAGCCAGCCGAGTACTTTTGTGGGTGTCCAT 549 GGCATGTTCACGATCAATTCCATTGGCCGGCTGGGGAACCAGATGGGCGAATACGCCACA CICITIGCACIGGCCAGGAIGAACGGACGGCITGCGITCATCCCCGCATCCATGCACAAC CIGCTCGCCCTCGCCCCAGCCCCCCAGCCTTCATCCAGCCTGCCATGCAGCC GCTCTAGCGCCCATCTTCAGGATCAGCCTCCCGGTGTTACACAGCGACACGGCCAAAAAG ATCCCATGGCAGAATTACCATCTCAACGACTGGATGGAGGAGCGTTACCGCCACATTCCG GGACACITTGTGCGCCTTCACGGGATACCCGTGCTCCTGGACCTTCTACCACCACCTGCGC GAGCCTGGCTGAACTCACCGGCTTCCTCTGGACCTTCTTCCACCACCTCGGG CCAGAGATCCTGAAGGAGTTCACCCTGCATGACCACGTGCGGGAGGAGGCGCCCAGGCCTTC GAGCAGATCCGCAGCGAGTTCACCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGGTA GTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCCGAGGTAGACAGGCAC Gaps Score 423.8; DB 24; Length 1269; Pred. No. 2e-108; 0: Mismatches 252; Indels 6; 39.7%; 591; Conservative Query Match Best Local Similarity 136 243 196 303 256 423 543 363 496 Matches δŽ g δý g Qγ g ŏ q ${\bf Q}$ Op Qqq ŏ

1082 722 699 782 729 789 606 903 849 730 GIGGIGTICGCGGGCAATGGTATTGAGGGGTCGCCAGCCAAGGACTTCGCGGTGCTCACC 723 GGGGCTTACCTCCAGCAGGCTATGGACTGGTTCCGGGGCCCGGTACGAAGCCCCCCTCTTT 670 GIGGITACAAGCAACGGIAIGGCCIGGIGCCGGGAGAACAITAAIGCITCCCGAGGAGA 550 GTGCGCCGAGGGGACTATGTGCATGTCATGCCTAATGTGTGGAAGGGCGTGGTGGCTGAC 663 GTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGAC CGGGGTTACCTGGAAAAGGCCCTGGATATGTTCCGGGCACGCTATTCATCTCCAGTCTTC 790 CAGIGCAACCACACCAICAIGACIAIIGGGACCIIIGGGAIIIGGGCIGCCIACCIGGCA 850 GGTGGTGATACCATCTACTTAGCCAACTACACCCTTCCGGATTCTCCGGTTCCTCAAAGTC 910 TITAAGCCAGAGCCAGCCTICCIACCCGAATGGGIGGGCATCCCTGCCGATCTCTCCCCA 1083 CTCCAGATG 1091 970 CICCITAAG 978 ŏλ g ŏ g QΫ́ qq δλ g δŽ qq ŏ qq δď

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/*tag= b /phenotype= "Confers resistance to F18

Socation/Qualifiers

/*tag= a /product= "FUT1"

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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Compugen Ltd.
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US-08-28-889A-1
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                                                                     GENERAL INCOMATION:
APPLICANT: EXIC H. Holmes et al.
APPLICANT: EXIC H. Holmes et al.
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE
TITLE OF INVENTION: GMI-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENTION: THERBOF
FILE REFERENCE: 8511-029
CURRENT APPLICATION NUMBER: US/09/298,885
CURRENT APPLICATION NUMBER: US/09/298,885
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 9.
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Pred. No. 2.2e-305;
Mismatches 0;
RESULT 1
US-09-298-886-9
Sequence 9, Application US/09298886
; Patent No. 6329170
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US-09-298-886-9
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APPLICANT: Eric H. Holmes et al.

APPLICANT: Eric H. Holmes et al.

TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE
TITLE OF INVENTION: GM.-SPECIFIC ALPHAI-2 FUCCSYLTRANSFERASE AND USES
TITLE OF INVENTION: THEREOF
FILE REPRENDANCE: 8511-029
CURRENT APPLICATION NUMBER: US/09/298,886
CURRENT APPLICATION NUMBER: US/09/298,886
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PALENTIN VET: 2.0
SEQ ID NO 7
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US-09-298-886-7
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                                                                                                                                                                                                                                                                                                                                                                                                       361 TACCGCCACATTCCGGGACACTTTGTGCGCTTCACGGGATACCCGTGCTCCTGGACCTTC
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                                                        1 CTCCAGCAGCGAATAGTGAAGCTCCAACCCCTGTCAGAGAAGGAATTACCGATGACGACT
                                                                       CAAATGTCCTCGGGAAACACAGAAAGCCCAGAGATGCGACGGGACAGCGAGCAGCATGGG
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 Length 1149;
 3; DB 4;
2.3e-305;
                            0; Mismatches
 Score 1068;
Pred. No. 2.
100.0%;
                            Conservative
                Similarity
 Query Match
Best Local Simi
Matches 1068;
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APPLICANT: ROUGUIER, SYLVIE
APPLICANT: GIORGI, DOMINIQUE
APPLICANT: GIORGI, DOMINIQUE
TITLE OF INVENTION: GDP-L-FUCOSE: BETA-D-GALACTOSIDE
TITLE OF INVENTION: 2-ALPHA-L-FUCOSYLTRANSFRASES, DNA SEQUENCES ENCODING THE
TITLE OF INVENTION: SAME, METHOD FOR PRODUCING THE SAME AND A METHOD OF
TITLE OF INVENTION: GENOTYPING A PERSON
      738 GCCTGGTGTCGCGAAAACATCAATGCCTCGCCGGCGATGTGTGTTTTGCCGGCAATGGC 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 AGCIGCGGGCATGTICACGATCAATTCCATTGGCCGGCTGGGGAACCAGAIGGGCGAAT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 AGCTCAGGGGGATGTGGACGATCAATGCAATAGGCCGCCTGGGGAACCAGATGGGCGAGT 298
                                             ATTGAGGGGTCGCCAGCCAAGGACTTCGCGCTGCTCACCCAGTGCAACCACACATCATG
                                                                  ACTATTGGGACCTTTGGGATTTGGGCTGCCTACCTGGCAGGTGGTGATACCATCTACTTA
                                                                                                                                               GCCAACTACACCCTTCCGGATTCTCCGTTCCTCAAAGTCTTTAAGCCAGAGGCAGCCTTC
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                                                                                                                                                                                                                                                                                   CTACCCGAATGGGTGGGCATCCCTGCCGATCTGTCCCCACTCCTTAAG
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STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.3%; Score 590.6; DB 1; 79.8%; Pred. No. 1.8e-164; 1ve 0; Mismatches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/08/395,800A
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TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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TELEPAX: (703) 413-2220
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 7:
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APPLICANT: LENNON, GREGORY
APPLICANT: ROUQUIER, SYLVII
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LENGTH: 2115 base pair:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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STRANDEDNESS:
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTCAGGATCAGCCTCCCGGTGTTACACAGGGACACGGCCAAAAAGATCCCATGGCAGAAT 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TICACGGGATACCCGTGCTCCTGGACCTICTACCACCACCTGCGCCCCAGAGATCCTGAAG 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 378 TACCACCTGAACGACTGGATGGAGGGGGGTACCGCCACATCCCGGGGGAGTACGTGCGC 437
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APPLICANT: SANDRILON.

APPLICANT: SANDRILON.

TITLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES

FILE REFERENCE: 30562.505W0

CURRENT APPLICATION NUMBER: US/09/254,077A

CURRENT FILING DATE: 1999-06-11

PRIOR PELICATION NUMBER: PO 1823

PRIOR FILING DATE: 1996-08-22

PRIOR APPLICATION NUMBER: PO 1823

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PATENT NOS: 12

SOFTWARE: PATENT NOS: 12

SOFTWARE: PATENT NOS: 12
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                      GCAAAAGGAGTCACTTGTTACGTCGCAGGAAGAGCCTTCTGATGGGAA 1149
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Score 612.8; DB 4;
Pred. No. 3.7e-171;
0; Mismatches 172;
                                                                                                                    Sequence 5, Application US/09254077A Patent No. 6399758
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80.68;
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Best Local Similarity 80.69
Matches 716; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Sus scrofa
                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         1043
                                                                                               US-09-254-077A-5
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130 CTGCGGGGCATGTTCACGATCAATTCCATTGGCCGGCTGGGGAACCAGATGGGCGAATAC 189
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CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
                                                                                                                                                                                               SOFTWARE PATENTIN STATE.

SOFTWARE PATENTIN BATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 28-FEB-1995
CLASSIFICATION: 435
CLASSIFICATION: 10FORMATION:
FELECOMMUNICATION: 1733 413-220
TELEFAX: (703) 413-3000
TELEFAX: (703) 413-220
TELEFAX: (703) 413-200
TELEFX: 248855 OPAT OR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

Query Match

48.4%; Score 516.6; DB 1;

Best Local Similarity 77.1%; Pred. No. 9.1e-143;

Matches 642; Conservative 0; Mismatches 189;
                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1144 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                          ZIP: 22202
COMPUTER READABLE FORM:
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LOCATION: 56..721
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FEATURE:
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US-08-395-800A-1
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5-ALPHA-LL-FUCOSYLTRANSFERASES, DNA SEQUENCES ENCODING THE
SAME, METHOD FOR PRODUCING THE SAME AND A METHOD OF
GENOTYPING A PERSON
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                                    ATGTGGGCCGAGGGGACTATGTGCATGCCTAATGTGTGGAAGGCGTGGTGGTG
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               188 ACGCCACACTCTTTGCACTGGCCAGGATGAACGGACGGCTTGCGTTCATCCCCGCATCCA
                                                                                        TGCACAACGCTCTAGCGCCCATCTTCAGGATCAGCCTCCCGGTGTTACACACAGCGACACGG
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APPLICANT: LOWE, JOHN B APPLICANT: LENNON, GREGORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROUQUIER, SYLVIE
GIORGI, DOMINIQUE
KELLY, ROBERT J
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APPLICANT: GLORGI, DO)
TITLE OF INVENTION: GI
TITLE OF INVENTION: SI
TITLE OF INVENTION: SI
TITLE OF INVENTION: SI
TITLE OF SEQUENCES: SI
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Length 1144;

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1023 TTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAAAGGAGAGACTTGTCTCCA 1082
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543 GAGCAGATCCGCAGCGAGTTCACCCTGCACCTTCACCTTCGGCAAGAGGCCCAGGGGGTA
                                                                                                                                                                                                                     610 CGGGGTTACCTGGAAAAGGCCCTGGATATGTTCCGGGCACGCTATTCATCTCCAGTCTTC
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                                                         CTGCGT -----GGTCTGCGGGTGAAIGGGAGCCAGCCGAGTACTTTGTGGGTGTCCAT
                                                                                603 CTGAGTTCCGTCTACCCCGCACAGGGAQCGCCCCAGCACCTTCGTGGGGGTCCAC
                                                                                                                                       550 GTGCGCCGAGGGGACTATGTGCATGTCATGCCTAATGTGTGGAAGGGCGTGGTGGCTGAC
                                                                                                                                                                               663 GTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTTGGAAGGGGGTGGTGGTGATGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/0820889A
Patent No. 5750176
GENERAL INFORMATION:
APPLICANT: Prieto, P., Smith, D., Cummings, R., Kopchick, J., IIILE OF INVENTION: Transgenic Production of Oligosaccharides TITLE OF INVENTION: Glycoconjugates
NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Diskette, 3.5 inch, 1.44 Mb storage IBM Compatible
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TELEPHONE: (614) 624-7080
TELEPHONE: (614) 624-3074
TELEX: No. 5750176e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: MS-DOS Version 6.0a
SOFTWARE: WordPerfect Version 6.0a
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/208,889A FILING DATE: 09-MAR-1994 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Donald O. Nickey
ADDRESSEE: ROSS Products Division
ADDRESSEE: Abbott Liaboratories
STREET: 625 Cleveland Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United States of America 2IP: 4315
COMPUTER READALLE FORM: MEDIUM TYPE: Diskette, 3:5 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1083 CTCCAGATG 1091
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                                                         496
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                                   790 CAGIGCAACCACACCAICAIGACTAIIGGGACCTIIGGGAITIGGGCIGCCIACCIGGCA 849
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            670 GIGGITACAAGCAACGGTAIGGCCIGGIGCCGGGAGAACAITAAIGCIICCCGAGGACAC 729
                                                                                        GIGGIGIICGCGGGCAAIGGIAITGAGGGGICGCCAGCCAAGGACIICGCGCIGCICACC 789
                                                                                                                                                                                                               900 CAGTGCAACCACCATCATCACGGGGCACCTTCGGGGTCTGGGGCGGCGTACCTCGCG 959
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GENERAL INFORMATION:
APPLICANT: Ridparth, Julia
APPLICANT: Ridparth, Julia
APPLICANT: Ridparth, Julia
APPLICANT: Wiseman, Barry
TITLE OF INVENTION: INTERACTIONS BETWEEN GENOTYPE AND DIET IN SWINE THAT
FITLE OF INVENTION: PREVENT E. COLI ASSOCIATED INTESTINAL DISEASE
FILE REFERENCE: 21419-90119
CURRENT APPLICATION NUMBER: US/09/151,592
CURRENT FILING DATE: 1999-09-18
NUMBER OF SEQ ID NOS: 4
SOFTWARRE: Patentin Ver. 2.0
SEQ ID NO 1
                                                                                                             GCTCTAGCGCCCATCTTCAGGATCAGCCTCCCGGTGTTACACAGGGGCGACACGGCCAAAAAG
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69.6%; Pred. No. 2.2e-115;
Live 0; Mismatches 252;
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Patent No. 6355859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 69.0
Matches 591; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: FUT1
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US-09-151-592-1
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Mukerji,

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APPLICANI: Prieto, P., Smith, D., Cummings, R., Kopchick, J., Mukerji, P., APPLICANI: Moremen, K., Pierce, J.
IILE OF INVENTION: Humanized Milk
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                                             436 CCAGAGATCCTGAAGGAGTICACCCTGCATGACCACGTGCGGGGAGGAGGCCCAGGCCTTC 495
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      512 GARCCITICCEGAAGCECTCTGGCITCCCCTGCTCTEGACTETCTTCCACCATCTCCGG 571
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ADDRESSEE: ROSS Products Division
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,122
FILING DATE: 09-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08433271
Patent No. 5891698
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     331
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                                                                                                             MOLECULE TYPE: Cloned cDNA representing the product of a MOLECULE TYPE: human genomic DNA segment DESCRIPTION: GDP-L-fucose- -D-galactoside 2-alpha-fucosyl-transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 GGCATGTTCACGATCAATTCCATTGGCCGGCTGGGGAACCAGATGGGCGAATACGCCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Epidermal Carcinoma Cell line
                                                                                                                                                                                                                FRAGMENT TYPE: Entire amino acid sequence provided. ORIGINAL SOURCE: Human Epidermal Carcinoma Cell line
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Journal of Biological Chemistry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                SEQUENCE CHARACTERISTICS:
LENGTH: 1155 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
IDENTIFICATION METHOD:
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INFORMATION FOR SEQ ID NO:
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DEVELOPMENTAL STAGE:
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   LIBRARY:
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ORGANISM:
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TISSUE TYPE:
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Matches
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APPLICANT: Lowe, John B. TITLE OF INVENTION: Method and Products For the Synthesis of TITLE OF INVENTION: Method and Products For the Synthesis of TITLE OF INVENTION: Oligosaccharide Structures on Glycoproteins, Glycolipids, TITLE OF INVENTION: or as Free Molecules, and For the Isolation of Cloned TITLE OF INVENTION: Genetic Sequences That Determine These Structur CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1051
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                                                                                   GGACACTITGIGCGCTICACGGGATACCCGTGCTCCTGGACCTTCTACCACCACCTGCGC
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1755 Jefferson Davis Highway, Suite 400
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, W
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/00699
FILING DATE: 19910214
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STATE: VAL.
TO: 22202
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ADDRESSEE:
STREET: 179
CITY: Arlin
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PCT-US91-00899-10
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OTHER INFORMATION: The encoded product of nucleotide SEQ ID NO:
OTHER INFORMATION: 1: is the enzyme, GDP-L-fucose- -D-galactoside 2-alpha-fucosy
OTHER INFORMATION: which has the amino acid sequence described in SEQ. ID NO:1:.
OTHER INFORMATION: is responsible for the synthesis of 2'-fucosyllactose.
AUTHORS: V.P. Rajan, et al.
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                                                                                                                                                                                                              MOLECULE TYPE: Cloned cDNA representing the product of a MOLECULE TYPE: human genomic DNA segment DESCRIPTION: GDP-L-fucose- -D-galactoside 2-alpha-fucosyl-transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 GGCATGTTCACGATCAATTCCATTGGCCGGCTGGGGAACCAGATGGGCGAATACGCCACA
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                                                                                                                                                                                                                                                                                                         Entire amino acid sequence provided. : Human Epidermal Carcinoma Cell line
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Pred. No. 8.5e-111;
0; Mismatches 258;
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VOLUME: 264
ISSUE:
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CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (614) 624-7080
IELEFAX: (614) 624-8074
TELEX: NO. 5891698e
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 base pairs
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ilarity 68.7%;
Conservative C
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CHROMOSOME/SEGMENT:
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                                                                                                                                                                                                     Unknown
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LIBRARY:
CLONE:
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UNITS:
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ORGANELLE:
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Best Local Simi
Matches 579;
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TELEFAX: (703) 413-220
TELEX: 24885 OPAT UNFORMATION FOR SEQ ID NO: 9:
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APPLICANT: LENNON, GREGORY
APPLICANT: ROUQUIER, SYLVIE
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Best Local Similarity 68.44
Matches 577; Conservative
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TYPE: nucleic acid
STRANDEDNESS: double
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CLASSIFICATION.
AUTONINY/AGENT INNEMATION:
NAME: LAVALLEYE Ph.D., Jean-Paul
REGISTRATION NUMBER: 31,451
FORTHAMEN NUMBER: 2363-021-55 PCT
                                                                 TELECOMMUNICATION INFORMER: 2503
TELEPHONE: (703)521-5940
TELEPAX: (703)486-2347
TELERX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHRRACTERISTICS:
LENGTH: 999 base pairs
TYRE: NUCLEIC ACID
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GDP-L-FUCOSE: BETA-D-GALACTOSIDE
2-ALPHA-L-FUCOSYLTRANSFERASES, DNA SEQUENCES ENCODING THE
SAME, METHOD FOR PRODUCING THE SAME AND A METHOD OF
GENOTYPING A PERSON
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GGTGGTGATACCATCTAGTTAGCCAACTACACCTTCCGGATTCTCCGTTCCTCAAAGTC
                                                                                                                           859 GGCGGAGACACTGTCTACCTGGCCAACTTCACCCTGCCAGACTCTGAGATC
                                                                                                910 TITAAGCCAGAGGCAGCCITCCTACCCGAATGGGTGGGCATCCCTGCCGATCTGTCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/395,800A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 405; DB 1; L
Pred. No. 7.4e-110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/395,800A
FILING DATE: 28-78EB-1995
CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/08395800A Patent No. 5807732 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ROUGUIER, SYLVIE
APPLICANT: GIORGI, DOMINIQUE
APPLICANT: KELLY, ROBERT J
TITLE OF INVENTION: GDP-L-FUCOS
TITLE OF INVENTION: 2-ALPHA-L-F
TITLE OF INVENTION: GRAE, METH
TITLE OF INVENTION: GROUTPING
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
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136 GGCATGTTCACGATCAATTCCATTGGCCGGCTGGGGAAACCAGATGGGCGAATACGCCACA 195
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Pred. No. 7.5e-110;
0; Mismatches 260;
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           storage
                                                                                                                                                                                                                                                                                                                                                                                             ALX-144.1PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE: Molecular cloning, sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1174 base pairs
TYPE: Nocleic Acid
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: CDNA to mRNA
DESCRIPTION: Human H-transferase
HYPOTHETICAL: No
ANTI-SENSE: NO
PUBLICATION INFORMATION:
AUTHORS: Larsen, R.D.
AUTHORS: Larsen, R.D.
AUTHORS: Nair, R.P.
AUTHORS: Nair, R.P.
AUTHORS: Nair, R.P.
AUTHORS: Nair, R.P.
AUTHORS: Lowe, J.B.
                                                                                                           APPLICATION NUMBER: PCT/US95/07554
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Academy of Sciences, USA
  MEDIUM TYPE: 3.5 inch, 750 Kb. COMPUTER: Dell 486/50 OPERATING SYSTEM: DOS 6.2 SOFTWARE: WOYGPERFECT 6.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                               08/278,282
                                                                                                                                                                                                 08/260,201
                                                                                                                                                                                                                                                                                                                                                              REGESTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255-1400
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/260,2
FLING DATE: June 15, 1994
CLASSIFICATION:
APPLICATION NUMBER: 08/278,2
FILING DATE: July 21, 1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 37.9%;
Best Local Similarity 68.4%;
Matches 577; Conservative 0
                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAGES: 6674-6678
DATE: SEP-1990
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                                                                                   316 ATCCCATGGCAGAATTACCATCTCAACGACTGGATGGAGGAGCGTTACCGCCACATTCCG
                                                                                                              453 ACGCCGTGGCGGAGCTGCAGCTTCACGATGTCGGAGGAGTACGCGGACTTGAGA
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GENERAL INFORMATION:
APPLICANT: Sandrin, Mauro S.
APPLICANT: Fodor, William L.
APPLICANT: Rother, Russell P.
APPLICANT: Squinto, Stephen P.
APPLICANT: McKenzie, Ian F. C.
TITLE OF INVENTION: Methods for Reducing
TITLE OF INVENTION: MPYPERCULE Rejection of Xenografts
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maurice M. Klee
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STATE: Connecticut
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CAGTGCAACCACACCATTATGACCATTGGCACCTTCGGCTTCTGGGCTGCCTACCTGGCT 1004
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Pred. No. 7.6e-110;
0; Mismatches 260;
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TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 24855 OPAT UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1199 base pairs
                                                                                                                                                                                                                                              37.98;
68.48;
                                                                                                                                                                                                                                                                                  Conservative
                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                         CDS
51..1145
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Best Local Similarity
Matches 577; Conserv
                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                             LOCATION:
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APPLICANT: ROUGUIER, SYLVIE
APPLICANT: GIORGI, DOMINIQUE
APPLICANT: KELLY, ROBERT J
TITLE OF INVENTION: GDP-L-FUCOSE: BETA-D-GALACTOSIDE
TITLE OF INVENTION: SAME, METHOD FOR PRODUCING THE SAME AND A METHOD OF
TITLE OF INVENTION: GENOTYPING A PERSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCGGAGACACTGTCTACCTGGCCAACTTCACCTGCCAGACTCTGAGTTCCTGAAGATC 1028
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                           GTGGTTACAAGCAACGGTATGGCCTGGTGCCGGGAACATTAATGCTTCCCGAGGAGAC 729
 CCAGAGATCCTGAAGGAGTTCACCCTGCATGACCACGTGCGGGAGGAGGACCAGGCCTTC 495
                                                                                         AGCGCCTACCTCCGGCAGGCCATGGTTCCGGGCACGGCACGAAGCCCCCGGTTTTC
                                                                                                                                                                                                                                                                                                   GTGCGCCGTGGGGACTATCTGCAGGTTATGCCTCAGCGCTGGAAGGGTGTGGTGGGGCGAC
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                                                                     CTGCGTGGTCTGCGGGTG-----AATGGGAGCCAGCCGAGTACTTTGTGGGGTGTCCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.30
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28-FEB-1995
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IBM PC compatible
YSTEM: PC-DOS/MS-DOS
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Patent No. 5807732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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CTC 1091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTC 972
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ZIP: 30309-4530
COMPUTER READABLE FORM:
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STATE: Georgia
COUNTRY: USA
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US-08-273-411-2
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2268;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,773B
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Pred. No. 1e-109;
                                                                                                                                                                                                                                                                            ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 SEVENTH STREET, N.W., SUITE 300
CITX: WASHINGTON
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03-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                          Sequence 4, Application US/08675773B Patent No. 6166288 GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                    APPLICANT: DIAMOND, LISA E
APPLICANT: LOGAN, JOHN S
APPLICANT: BYRNE, GUERARD W
APPLICANT: SHARMA, AJAY
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68.4%;
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202-737-3528
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Best Local Similarity 68.4
Matches 577; Conservative
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                  1125 CTC 1127
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970 CTC 972
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STATE:
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1469 GGGGGAGACACTGTCTACCTGGCCAACTTCACCTGCCAGACTCTGAGTTCCTGAAGATC 1528
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436 CCAGAGATCCTGAAGGAGTTCACCCTGCATGACCACGTGCGGGAGGAGGCCCCAGGCCTTC 495
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APPLICANT: Falk, Per
APPLICANT: Falk, Per
APPLICANT: Gardon, Jeffrey I.
TITLE OF INVENTION: Animal Model for Gastro-Intestinal
NUMBER OF INVENTION: Disease
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0, Version #1.25
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CURRENT APPLICATION DATA:
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1100 Peachtree Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08273411 Patent No. 5625124
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COMPUTER: IBM PC compatible
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                                                                                                 496 CIGCGIGGICIGCGGGIG
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ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,3
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                          1057
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      1058 GGCGGAGACACTGTCTACCTGGCCAACTTCACCTGCCAGACATCTGAAGATC
                                                                                                                                                            1118 TITAAGCCGGAGGCGGCCTTCCTGCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               METHOD OF PRODUCING TRANSGENIC ANIMALS FOR XENOTRANSPLANTATION. . . 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 405, DB 4; I
Pred. No. 1.3e-109;
0; Mismatches 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEE: BROWDY AND NEIMARK, P.L.L.C. : 419 SEVENTH STREET, N.W., SUITE 300 WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: DIAMOND=1A TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                     US/08675773B
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: LOGAN, JOHN S
APPLICANT: BYRNE, GUERARD W
APPLICANT: SHARNA, AJAX
TITLE OF INVENTION: METHOD OF
TITLE OF INVENTION: FOR XENOT
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28,005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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68.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                             LISA E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION: NAME: COOPER, IVER P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3791 base pairs
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Best Local Similarity 68.45
Matches 577; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application Patent No. 6166288
                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: DIAMOND,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                       1178 CTC 1180
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0; Mismatches 260;
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Proc. Nat'l Acad.
TELEPHONE: (404) 815-6508
TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 2: SEGUENCE CHARACTERISTICS:
LENGTH: 3373 base pairs
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68.48;
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LOCATION: 104..1201
OTHER INFORMATION: /not
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2413 GCCTGGCCCGGGTATTCCGCATCACCCTGCCCGTGCTGGCCCAGAAGTGGACAGCCGC 2472
                                                                                 2533 GAICCITTCCIGAAGICTCTGGCTTCCCCTGTCTTGGACTTTCTTCCACCAICTCCGG 2592
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Search completed: May 26, 2003, 11:58:34 Job time : 60.2896 secs

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Compugen Ltd.
 GenCore version
Copyright (c) 1993 - 2003
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Run on:

May 26, 2003, 11:58:37 ; Search time 163.789 Seconds (without alignments) 8610.191 Million cell updates/sec

US-10-040-863-9 1068 Title: Perfect score:

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Scoring table: Seguence:

IDENTITY_NUC Gapoxt 1.0

828747 segs, 660231138 residues Searched:

length: 0 length: 20000000000 Minimum DB seq Maximum DB seq

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published_Applications_NA:*

/ Cgn2_6/ptodata/1/pubpna/US07_pUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US06_wBP_UB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

	Description		Segmence 9 Annli	n a	11		Sequence /, Appli	, K				, (10	Sequence 12, Appr	τ - μ	, ,	sednence 29, Appl	Sequence 29, Appl	23	TAME 100 CONTROL		Sequence 23, Appl	Sequence 26, Appl
	ID		US-09-999-672-9	US-10-040-863-9	US-09-999-672-7	US-10-040-863-7	US-09-051-034A-1	US-09-954-456-45	US-09-954-456-1621	US-09-969-347-234	US-09-051-034A-3	US-09-844-268-12	US-09-844-705-12	US-10-105-963-9	US-09-863-475b-c	TC-00-000-01-00		US-10-040-863-29	US-09-999-672-23	TG-00-000-01	02-270 666 60 00	US-10-040-863-23	US-10-040-863-26
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Sequence 20, Appl Sequence 14, Appl Sequence 14, Appl Sequence 17, Appl Sequence 17, Appl Sequence 98, Appl Sequence 98, Appl Sequence 16, Appl Sequence 113, Appl Sequence 113, Appl Sequence 159, Appl Sequence 159, Appl Sequence 159, Appl Sequence 28, Appl Sequence 19, Appl Sequence 28, Appl Sequence 19, Appl	24 78, 78, 19,
US-109-999-672-20 US-10-040-863-20 US-009-999-672-14 US-109-999-672-14 US-10-040-863-14 US-10-10-683-14 US-10-10-863-17 US-09-764-870-98 US-09-764-870-98 US-09-764-870-98 US-09-764-8713 US-10-051-643-13 US-10-051-643-159 US-10-051-643-159 US-10-051-643-159 US-10-051-643-159 US-10-051-643-159 US-10-051-643-159 US-10-051-643-159 US-10-059-672-28 US-10-040-863-25 US-10-10-040-863-25 US-10-10-44-1312	JS-09-880-107- S-10-184-644-7 S-10-184-634-7 S-08-900-220C-
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ALIGNMENTS

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APPLICANT: Eric H. Holmes et al.
APPLICANT: Eric H. Holmes et al.
TITLE OF INVENTION: UGCLEIC ACIDS AND PROTEINS OF A RAI GANGLIOSIDE
TITLE OF INVENTION: GMI-SPECIFIC ALPHA1-2 FUCOSYLTRANSFERASE AND USES
FILE REFERENCE: 8511-029
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                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/999,672
CURRENT FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: US/09/298,886
PRIOR FILING DATE: 1999-04-26
                                     Sequence 9, Application US/09999672
Patent No. US20020127655A1
                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Rattus norvegicus
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SOFTWARE: Patentin Ver. 2.0
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US-09-999-672-9
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PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 29
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Sequence 9, Application US/10040863

Sequence 9, Application US/10040863

GENERAL INFORMATION:

APPLICANT: Eric H. Holmes et al.

APPLICANT: Eric H. Holmes et al.

TITLE OF INVENTION: NUCLBIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE

TITLE OF INVENTION: GMI-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERASE AND USES

TITLE OF INVENTION: US/10/040,863

CURRENT APPLICATION NUMBER: 09/299,886

US-10-040-863-9

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The invention relates to rat GMI-specific alphal-2fucosyltransferase (alphal-2FucT) enzyme and its corresponding nucleic acid. This nucleic acid is specific for a carbohydrate moiety found in ganglioside GMI, a terminal galactose betal-3R-acetylgalactosamine (Galbetal-3GalNAC) saccharide. Alphal-2FucT DNA is useful for producing rat alphal-2FucT protein by recombinant techniques. Alphal-2FucT DNA is useful for the preparative synthesis of fucosyl containing glycolipids, glycoproteins, glycolipoproteins and oligosaccharide, and for preparing fucosyl-GMI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat, alphal-2fucosyltransferase, alphal-2FucT; antisense therapy; galaatose batal.3N-acetylgalaatosamine; Galbetal-3GalNac, glycollpid; gylycoprotein; glycollpoprotein; oligosaccharide; fucosyl-GM1; cancer; gene therapy; oncogenic transformation; cytostatic; ganglioside; GM1;
                                         GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS
                                                                                                       RGDVVFAGNG1EGSPAKDFALLTQCNHTIMT1GTFG1WAAYLAGGDT1YLANYTLPDSPF
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/note= "Intracellular/Transmembrane domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New rat ganglioside GMI-specific alphal-2Fucosyltransferase, useful for preparation of fucosyl GMI which is useful as a nutritional composition or immunotherapeutic for cancer and neurological diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is useful for inducing an immunotherapeutic or immunosuppressive action against cancer, neurological disease or small cell lung carcinoma.
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                                                                                                                                                                                                                                                              Rat; alphal-2fucosyltransferase; cytostatic; neuroprotective; nootropic; gene therapy; Fucalphal-2Galbetal-3GalNAc; immunotherapy; immunosuppression; cancer; neurological disease;
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301 LKVFKPEAAFLPEWVGIPADLSPLLKALTPACPRSHFELKAKGVTCYVAGRAF 353
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                                                                                                    AAB36104 standard; Protein; 380
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Best Local Similarity 100.0
Matches 353; Conservative
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                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-APR-1999;
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                                                                                                                                                                                   19-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Holmes EH,
                                                                                                                                            AAB36104;
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                                                         RESULT 3
AAB36104
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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26-FEB-1998
                                                                                                                  Modified-site
                                                                                                                                                                  Modified-site
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                                                WO9807837-A1
                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Porcine secretor transferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YRHIPGHFVRFTGYPCSWIFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glycosyltransferase; FUT2; pig; epitope; antige
c animal; xenotransplantation; organ transplant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                380 AA;
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                                                                                                                    /note=
                                                                                                                                                                  /note≃
279..2
                                                                                                                                                                                                                  /note=
251..2
                                                                                                                                                                                                                                                                                                           /note= "transmembrane 27..340
                                                                                                                                                                                                                                                              /note= "C-terminal domain"
185..187
                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                        /note=
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                                                                                      N-glycosylated
                                                                                                                                         N-glycosylated'
                                                                                                                                                                                      N-glycosylated'
                                                                                                                                                                                                                                    N-glycosylated'
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SE or FUT2), a type II integral membrane profession affinity of or type I and type III substrates. Its amino acid sequence was deduced from the nucleotide sequence of a genomic DNA clone (see AAV2903) isolated from a pig liver library on the basis of homology to human FUT2 cDNA. Pig FUT2 shows 83.2% identity with human FUT2. Expression of a glycosyltransferase, such as porcine Se, in a tissue results in reduced expression of unwanted carbohydrate epitopes on the tissue, especially porcine heart, liver, kidney or pancreas, rendering it more suitable for transplantation, i.e. less immunogenic and of increased immunological acceptability. A claimed method of producing a cell from a donor species that is immunologically acceptable to a recipient species involves reducing recognised as non-self by the recipient by expressing a nucleic acid for a glycosyltransferase such as porcine Se in the cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 267;
                                                AAW53101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unwanted carbohydrate epitope(s) on tissues intended for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid encoding glycosyitransferase able to compete w second such enzyme - particularly used to reduce expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McKenzie
                                                                                                                                                                                                                                                                                                                                  134
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                                                                                                                                                                                                                                                                                      GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS
                                                                                                                                                                                                                                                                                                                                                                                                                   GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWONYHLNDWMEER 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM 60
                                                                                                                                LKLFKPEAAFLPEWIGIEADLSPLLK
                                                                                                                                                             LKVFKPEAAFLPEWVGIPADLSPLLK
                                                                                                                                                                                                RGDVVFAGNGIEGSPAKDFALLTQCNHTVMTIGTFGIWAAYLAGGETIYLANYTLPDSPF
                                                                                                                                                                                                                             RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF
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                                                                                                                                                                                                                                                                                                                                                                                              GEYATLYALARMNGRPAFIPPEMHSTLAPIFRITLPVLHASTARRIPWQNYHLNDWMEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LQQRMVKIQP--TWELQMVTQVT---TESP----SSPQLKGMWTINAIGRLGNQM
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                                                standard;
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                                             Protein;
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81.9%;
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Pred. No. 1
                                              AA
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1.2e-147;
nes 19;
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(first entry)

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GVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIFVVTSNGMAWCRENIJTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Column 45~50; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding fucosyltransferase enzyme
                                AA.
                             AAW69332 standard; Protein; 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ġ
                                                                                                                                                                                FUT2; nonsecretor genotyping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lennon
                                                                                                                                                                                                                                                                                                     95US-0395800.
                                                                                                                                                                                                                                                                                                                                   95US-0395800.
                                                                                                                      Human Sec2 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kelly RJ,
                                                                                                                                                                                                                                                                                                                                                                           KELLY R J.
LENNON G.
LOWE J B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-520127/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 258; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                        ROUQUIER S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        343 AA;
                                                                                                                                                                                                                                                                                                                                                             GIORGI D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAV58323
                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                     28-FEB-1995;
                                                                                                                                                                                                                                                                                                                                   28-FEB-1995;
                                                                                       20-NOV-1998
                                                                                                                                                                                                                                          US5807732-A.
                                                                                                                                                                                                                                                                       15-SEP-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ď,
                                                            AAW69332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                               (GIOR/)
                                                                                                                                                                                                                                                                                                                                                                              (KELL/)
                                                                                                                                                                                                                                                                                                                                                                                                                          (ROUQ/)
                                                                                                                                                                                                                                                                                                                                                                                                         LOWE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Giorgi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197
   RESULT 7
                  AAW69332
                                             δŽ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δà
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ωp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QY
                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents pig secretor used in an example of the present invention. The present invention describes nucleic acids (NA) encoding a chimaric glycosyltransferase. The NAs comprises a catalytic domain of a first glycosyltransferase (GT) and a localisation signal of a second GT, whereby when the NA is expressed in a cell and where the chimaric enzyme is located in an area of the cell where it is able to compete for substrate with a second GT, resulting in reduced levels of a product from the second GT, The NAs can be used to produce cells and organs with desired glycosylation patterns. Products and methods of the present invention can be used to reduce the levels of undesirable epitopes in cells, tissues or organs which may be used in transplantation or gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding chimeric glycosyltransferases - used for altering carbohydrate levels on the surface of cells, useful in gene therapy and transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 YRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 340;
                          Plg; secretor; chimeric; glycosyltransferase; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.4%; Score 1430; DB 19;
81.9%; Pred. No. 1.2e-147;
tive 26; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LKVFKPEAAFLPEWVGIPADLSPLLK 326
                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Fig 6; 51pp; English.
                                                                                                                                                                                        96US-0024279.
                                                                                                                                                             97WO-AU00492
                                                                                                                                                                                                                                                                    MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        267; Conservative
                                                                                                                                                                                                                                      (AUST-) AUSTIN RES INST.
                                                                                                                                                                                                                                                                                               WPI; 1998-159170/14.
N-PSDB; AAV21639.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             340 AA;
                                          transplantation.
                                                                                                                                                                                                                                                                   McKenzie IFC,
                                                                                                   W09805768-A1
                                                                                                                                                                                        21-AUG-1996;
02-AUG-1996;
secretor
                                                                                                                                                            01-AUG-1997;
                                                                                                                               12-FEB-1998
                                                                       Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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Best Local $
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Matches

g δ q ŏ qq 181 194 241 254 301

 $\delta \lambda$

Q D δ Dp.

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This sequence is the human Sec2 protein of the invention. The DNA encodes a alpha(1,2) fucosyltransferase and is the Secretor alpha(1,2)fucosyltransferase locus, that cross Appridises with the H blood group alpha(1,2)fucosyltransferase gene. The DNA is useful for producing a recombinant human GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase (FUT2) which can be used for genotyping an individual as a secretor or nonsecretor as it is known that nonsecretors homozygous for a mutant allele of the FUT2 gene that has a stop codon in the position corresponding to amino acid 143.
Sec2; alpha(1,2) fucosyltransferase; H blood group; secretor genotyping; GDP-L-fucose;beta-D-galactoside 2-alpha-L-fucosyltransferase; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVYTSNGMAWCRENINAS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nonsecretor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.1%; Score 1386.5; DB 19; Length 343; 79.1%; Pred. No. 7.3e-143; ive 26; Mismatches 31; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - useful for producing
on as secretor or nonse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lowe JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       recombinant enzyme and genotyping person
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Page

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WPI; 1991-267151/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycosyltransferase
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Best Local Similarity
Matches 195; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAR13751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-DEC-1990;
14-FEB-1990;
14-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VIND ( IMNU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9112340-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR13751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lowe JB;
                    11
                                                                                                                                                     180
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                                                                                                                                                                                                                                                                                 257
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                                                                121
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М
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is given in a specification relating to a rat ganglioside GM_1-specific alphal-2fucosyltransferase protein. The protein or its callular fraction is useful for synthesis of a molecule comprising Fucalphal-2Galbetal-3GalNac, a glycolipid, glycoprotein, glycolipoprotein or a free oligosaccharide comprising Fucalphal-2Galbetal-3GalNac.
The method involves contacting alphal-2fucosyltransferase with GDP-fucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New rat ganglioside GMI-specific alphal-2Fucosyltransferase, useful for preparation of fucosyl GMI which is useful as a nutritional composition or immunotherapeutic for cancer and neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                          neuroprotective; nootropic; gene therapy; Fucalphal-2Galbetal-3GalNAc; immunotherapy; immunosuppression; cancer; neurological disease; small cell lung carcinoma.
                                             257 HGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLTGGDTIYLANYTLPDSPF 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEYATLFALARMNGRLAFIPASMHNALAPIFRISLFVLHSDTAKKIPWQNYHLNDWMEER 120
                      241 RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and a molecule or glycolipid, glycoprotein, glycolipoprotein or oligosaccharide having a terminal Galbetal-3GalNAc group. It is also useful for synthesis of fucosyl-GML! by contacting the protein with GDP-fucose and ganglioside GML! The obtained glycoproteins, glycolipids and oligosaccharides are useful as nutritional compositions and fucosyl-GML! is useful for inducing an immunotherapeutic or immunosuppressive action against cancer, neurological disease or small cell lung carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOORIVKLOPLSEKELPMTTOMSSGNTESPEMRRDSEOHGNGELRGMFTINSIGRLGNOM 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----QIPVLASTSKALGPSQLRGMWTINAIGRLGNQM 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.6%; Score 1376; DB 2
78.9%; Pred. No. 1e-141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PACI-) PACIFIC NORTHWEST CANCER FOUND.
                                                                                                                                  LKVFKPEAAFLPEWVGIPADLSPLLK 326
                                                                                                                                                                                                                                                          AAB36106 standard; Protein; 344 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example; Fig 3B; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                          Human Sec2 catalytic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US07384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US07384
                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 VOORLAKIOAM--WELPV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sherwood AL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-687262/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200064464-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-APR-1999;
                                                                                                                                                                                                                                                                                                                                               19-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Holmes EH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
                                                                                                                                                                                                                                                                                                        AAB35106;
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137 YRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHDHVREEAQKFLRGLQVNGSRPGTF 196
                                                                                                            VGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINA 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The amino acid sequence codes for a protein capable of functioning as a GDP- Fuc: Deta-D-Gal alpha(1,2)- fucosyltransferase. The functional protein is represented by amino acids 33 to 365. The enzyme produced by the DNA sequence can be used in enzymatic fucosylation of chain-terminating galactose residues on lactoseamine or neolacto type beta-D-galactoside to alpha-2-L-fucose residues. See also ARK13749-R13752.
                                                                                                                                          SRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSP
YRHI-PGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolation of gene conveying post-translational characteristic e.g. the presence of soluble or membrane bound oligo or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 4e-106; /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDP-Fuc:beta-D-galactoside alpha(1,2)-fucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.5%; Score 1051.5;
63.3%; Pred. No. 4e-1
tive 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polysaccharide or glycosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                            FLKVFKPEAAFLPEWVGIPADLSPLLK 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 3; 155pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR13751 standard; Protein; 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90US-0627621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    900S-0479858.
900S-0480133.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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Length 365;

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203 238 263

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RESULT 10 AAR80154

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59 GTAMGPNASSSCPQH-PASLSGTWTVYPNGRFGNQMGQYATLLALAQLNGRRAFILPAMH 117
                                                                                                                                                                                                                                                              RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA 202
                                                                                                                                                                                                                                                                                                                                                     85 NALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New transgenic non-human mammal milk prods - contg. heterologous components produced as secondary gene prods. of an heterologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDP-L-fucose-beta-D-galactoside 2-alpha-fucosyltransferase, glycosyltransferase; glycosylation; oligosaccharide; glycoprotein; glycolipid; transgenic animal: cattle; milk.
                                                                                                                                                                                                                                                                                                                                                                                                                                            25 GNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMH
                                                                                                                                                                                                                                                                                                                                                                                                                   203 DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263 TQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2-Alpha-fucosyltransferase (AAR70422) is encoded by a cDNA clone (AAR01083) isolated from a human epidermal carchoma A31 library. The enzyme can be expressed in the milk of a transgenic mammal, esp. cow. This allows large-scale prodn. of oligosaccharides and
                                                             Score 1051.5; DB 16;
Pred. No. 4e-106;
'; Mismatches 73; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mukerji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . Kopchik JJ, Moremen KW, Prieto PA, Smith DF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 62-64; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR70422 standard; Protein; 365 AA.
                                                           Query Match
Best Local Similarity 63.3%; Pre
Matches 195; Conservative 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95WO-US00967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-FEB-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2-Alpha-fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-328284/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ABBO ) ABBOTT LAB.
                    365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               323 PLLKALTP 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      358 PLWTLAKP 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAT01083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cummings RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JAN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR70422;
                      Sequence
                                                                                                                                                                                                                                                                                                                            145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDP-L-fucose-beta-D-galactoside 2-alpha-fucosyl-transferase (Fuc-T) is encoded by CDMA (AAO98461) isolated from a human epidermal carcinoma cell line. The enzyme is responsible for the synthesis of 2'-fucosyllactose, one of the oligosaccharides in human milk. Other products of Fuc-T include glycoprotiens contg. beta-linked terminal galactose residues which can be fucosylated by Fuc-T. This DNA can be used to produce non-human transgenic mammals able to produce secondary gene products, e.g. oligosaccharides, in their milk. The transgenic mammals milk blochemically resembles human milk. This humanised milk can be used in the prepn. of an enteral nutritional product useful in the nutritive maintenance of an animal.
                                                                                                                                                                                                                  262
                                                                                                                                                                                                                                                              297
                                                                                                                                                                                                                                                                                                          TQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS 322
GTAMGPNASSSCPQH-PASLSGTWTVYPNGRFGNQMGQYATLLALAQLNGRRAFILPAMH 117
                                                                                                                              RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA 202
                                                                                                                                                                                                                                                                                                                                                 TQCNHTIMTIGTFGFWAAYLAGGDTVYLANFTLPDSEFLKIFKPEAAFLPEWVGINADLS 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDP-L-fucose-beta-D-galactoside 2-alpha-fucosyl-transferase; Fuc-T; synthesis; 2'-fucosyllactose; oligosaccharide; human milk; non-human transgenic mammal; secondary gene product.
                                                                    Prodn. of human:ised milk by non-human transgenic mammal - by inserting heterologous gene encoding human catalytic entity which produces oligo:saccharide(s) and glyco:conjugate(s) into mammal's
                                           NALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHL
                                                                                                                                                                     REQIRREFILHDHLREEAQSVLGQLRLGRTGDRPRIFVGVHVRRGDYLQVMPQRWKGVVG
                                                                                                                                                                                                                  DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALL
                                                                                                                                                                                                                                         GDP-L-fucose-beta-D-galactosidase alpha-1,2-fucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
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Smith DF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 62-64; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR80154 standard; Protein; 365 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95WO-US00926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-336739/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                        358 PLWTLAKP 365
                                                                                                                                                                                                                                                                                                                                                                                            PLLKALTP 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAQ98461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cummings RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-MAR-1994;
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Example 1; Page 45-47; 69pp; English
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15-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                              AAR90572,
                                            Sequence
                                                             Query Match
                                                                      Local
                                                                                                                                                                                                                                                                                                                            RESULT 13
AAR90572
                                                                               Matches
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                                                                                                                                                                                                                           AALAPVFRITILPVLAPEVDSRIPWRELQLHDWASEEYADLRDPFLKLSGFPCSWIFFHHL 177
                                                                                                                                                      262
                                                                                                                                                                                         TQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS 322
                                                                                                         NALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFIGYPCSWTFYHHL 144
                                                                                                                                            RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA 202
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alpha-1,2-fucosyltransferase (AAR70421) is encoded by a cDNA clone
                                                                      GNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMH
                                                                                  DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALL
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                                                                                                                                                                                                                                                                                                                                                                                       GDP-L-fucose-beta-D-galactoside 2-alpha-fucosyltransferase; glycosyltransferase; oligosaccharide; glycoprotein; glycolipid; transgenic animal; cattle; glycosylation; milk.
                                   DB 16; Length 365;
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                                                    73; Indels
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for prodn. of
in the milk,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mukerji
                                   55.5%; Score 1051.5; DB 63.3%; Pred. No. 4e-106; Live 37; Mismatches 7
glycosylated proteins and lipids in the milk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transgenic animal expressing heterologous metabolite prodn esp. glycosyltransferase oligosaccharide(s) and glyco-conjugate(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kopchik JJ, Moremen KW, rieto PA, Smith DF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 62-64; 84pp; English.
                                                                                                                                                                                                                                                                                                                    AAR70421 standard; Protein; 365 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95WO-US01147
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                                                                                                                                                                                                                                                                                                                                                                        2-Alpha-fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       foods, pharmaceuticals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prieto PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-328279/42.
N-PSDB; AAT01082.
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                                            al Similarity
195: Conserv
                                                                                                                                                                                                                                                                      PLWTLAKP 365
                  365 AA
                                                                                                                                                                                                                                                      PLLKALTP 330
                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                    AAR70421;
                   Sequence
                                    Query Match
                                                                                                                                                                                                                                                                                                  RESULT 12
AAR70421
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21
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263 TQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 TQCNHTIMTIGTFGFWAAYLAGGDTVYLANFTLPDSEFLKIFKPBAAFLPEWVGINADLS 357
                                                                                                                                                                                                                                                                                                                                                                                                                                      RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMBERYRHIPGHFVRFTGYPCSWIFYHHL 144
                                                                                                                                                                                                                                                                                                25 GNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMH 84
(AAT01082) isolated from a human epidermal carcinoma cell line A431 cDNA library. The enzyme can be expressed in the milk of a transgenic mammal, esp. cow. This allows large-scale prodn. of oligosaccharides or glycosylated proteins and lipids in the milk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203 DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALL
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by introducing a vector expressing fucosyl:transferase into the
cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H-transferase, xenograft hyperacute rejection; transplantation; glycosyltransferase; galactose alpha(1,3) galactose.
                                                                                                                                                                                          DB 16; Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Squinto
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                                                                                                                                                                                                                                            73;
                                                                                                                                                                                       55.5%; Score 1051.5; DB 63.3%; Pred. No. 4e-106; Live 37; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rother RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR90572 standard; Protein; 365 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95WO-US07554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94US-0278282
94US-0260201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fodor WL, Mckenzie IFC,
                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                   al Similarity
195; Conserv
                                                                                                                                        365 AA;
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203 DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALL 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The human H-transferase (AAR90572) product of a cDNA clone (AAT12238) prepd. from human epidermoid carcinoma cells (ATCC CRL 155 A-431) can be expressed in xenogeneic organs, tissues and cells using a vector such as pApEx-1 (AAT1239). This results in decreased expression of the non-human antigen galactose alpha(1,3) galactose on the surface of the organs etc. so that hyperacute rejection is reduced upon transplantation to humans.
                                                                                                                                                                                                                                                                                              NALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGGHFVRFTGYPCSWTFYHHL 144
                                                                                                                                                                                                                                                                                                                    145 RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA 202
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                 25 GNTESPEMREDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMH 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human GDP-L-fucose:beta-D-galactoside-2-alpha-L-fucosyltransferase; alpha 1,2 FT; transgene; transgenic mouse; animal model; intestinal adhesion; Helicobacter pylori infection; stomach; small intestine; gut; epithelial cell; surface receptor; carbohydrate antigen; gastritis; peptic ulcer; neoplasia; gastric adenocarcinoma; Lewis antigen; fucosylation.
                                                                                                                                                                                                                                                               59 GTAMGPNASSSCPQH-PASLSGTWTVYPNGRFGNOMGQYATLLALAQLNGRRAFILPAMH
                                                                                                                                                                                                                                                                                                                                                                                  Score 1051.5; DB 17; Length 365; Pred. No. 4e-106; 37; Mismatches 73; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human alpha 1,2 fucosyltransferase (EC 2.4.1.69).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW23805 standard; Protein; 365 AA.
                                                                                                                                                                      Query Match 55.5%;
Best Local Similarity 63.3%;
Matches 195; Conservative 37
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                                                                                                                                          365 AA;
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A carried ranspance and the control of the control of the control of a carried carried calls, the enzyme human GDP-L-fucose: beta-D-galactoside 2-falpha-L-fucosyltransferase (also called alpha 1,2 FT) or human GDP-L-fucose: beta-D-N-acetylalucosamide 3/4-alpha-L-fucosyltransferase (also called alpha 1,3/4 FT). The enzyme is expressed under the control of a gut epithelial cell-specific promoter and Helicobacter pylori adherse to the transgenic cells. The transgenic mouse and intestinal epithelial cells from it are useful as models for screening compounds for the ability to inhibit adhesion of H. pylori to gut epithelial cells. The present sequence represents human alpha 1,2 FT and was published by Larsen et al., Proc.Natl.Acad.Sci.USA, 87:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA
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                                                                                                                                                                                                                                                                                                                                                                                            55.5%; Score 1051.5; DB 18; Length 365; 63.3%; Pred. No. 4e-106; ative 37; Mismatches 73; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alpha(1,2)-fucosyltransferase; glycosylation; oligosaccharide;
             Animal model for Helicobacter pylori infection - comprising transgenic mouse expressing human enzyme promoting intestinal
                                                                                                                      transgenic mouse expresses, in its intestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253
                                                                                    Example 1; Columns 13-16; 24pp; English
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Matches 195; Conservative
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AAW13640
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Search completed: May 27, 2003, 15:06:16 Job time: 45.7707 secs

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RESULT' 1
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                                                               (without alignments) . 715.625 Million cell updates/sec
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Sequence 12,
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Sequence 11,
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Compugen Ltd.
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US-08-293-411-1
US-08-295-8008-6
US-08-395-8008-6
US-08-995-8008-10
US-08-696-731-6
US-09-042-531-6
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US-09-204-0778-11
US-09-21-0778-11
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US-09-254-0778-9

US-09-254-0778-12

US-09-254-0778-12

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US-08-208-897A-33
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  GenCore version
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Maximum Match 100%
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Patent No. 5470718
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Sequence 10, Application US/09298886
Sequence 10, Application US/09298886
GENERAL INFORMATION:
APPLICANT: Eric H. Holmes et al.
APPLICANT: Eric H. Holmes et al.
TITLE OF INVENTION: UNCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 8511-029
GURRENT APPLICATION NUMBER: US/09/298,886
CURRENT FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
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US-08-539-005-33
US-09-260-598-35
US-07-906-349A-6
US-08-220-151-22
US-08-413-118-22
US-08-413-446-22
S470718-3-446-22
5470718-3-446-22
US-08-208-897A-6
US-08-539-005-6
US-08-539-005-6
US-08-815-176-3
US-08-815-176-4
US-08-815-176-4
US-09-311-743-6
US-09-311-743-6
US-09-311-743-6
US-09-311-743-6
US-09-911-743-6
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Matches 353; Conservative 0
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, ORGANISM: Rattus norvegicus
US-09-298-886-10
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Conservative
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Matches 267;
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           Sequence 8, Application US/09298886
Patent No. 6329170
BATENT No. 6329170
APPLICANT: Eric H. Holmes et al.
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAT GANGLICSIDE
TITLE OF INVENTION: GMI-SPECIFIC ALPHAI-2 FUGOSYLTRANSFERASE AND USES
TITLE OF INVENTION: THEREOF
FILE REPERBRES: 8511-029
CURRENT APPLICATION NUMBER: US/09/298,886
CURRENT FILING DATE: 1999-04-26
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SANDRIN, MAURO S.
APPLICANT: MCKENZIE, IAN C. F.
APPLICANT: MCKENZIE, IAN C. F.
TITLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
FILE REFERENCE: 30562.505W0
CURRENT APPLICATION NUMBER: 105/09/254,077A
CURRENT FILING DATE: 1999-06-11
PRIOR PLILOR DATE: 1999-06-12
PRIOR PLILOR DATE: 1999-08-22
PRIOR PLILOR DATE: 1999-08-22
PRIOR PLILOR DATE: 1996-08-23
PRIOR PLILOR DATE: 1996-08-23
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                                                                                                                                                                                                                                                                                                              DB 4; Length 380;
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; Pred. No. 1.8e-210;
0; Mismatches 0;
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No. 1.le-156;
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Pred.
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100.0%;
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81.9%;
                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-298-886-8
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Best Local Similarity 100.0
Matches 353; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
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Best Local Similarity
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US-09-298-886-8
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GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER.120
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    Gaps
                                         1 LQQRIVKLQPLSEKELPMITQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM 60
                                                                                      -----SSPQLKGMWTINAIGRLGNQM 73
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APPLICANT: SANDRIN, MAURO S.
APPLICANT: MACENQIES, IAN C. F.
TITLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
FILE REFERENCE: 30562.505WO
                                                                                                                                                                                                                                                                                                              GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS
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  19; Indels
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81.9%; Pred. No. 1.1e-156;
iive 26; Mismatches 19;
Mismatches
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                                                                                   28 LQQRMVKIQP--TWELQMVTQVT---TESP-
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26;
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FILE REFERENCE: 8511-029
CURRENT APPLICATION NUMBER: US/09/298,886
CURRENT FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTUM VOY: 2.0
                      317 LKIFKPEAAFLPEWTGIAADLSPLLK 342
301 LKVFKPEAAFLPEWVGIPADLSPLLK 326
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; Patent No. 6329170
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SEQ ID NO 8
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Matches 258; Conserv
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US-09-254-077A-8
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APPLICANT: ROUGUIEN, SYLVIE
APPLICANT: GOOGUIEN, SYLVIE
APPLICANT: GOOGUIEN, DOMINIQUE
APPLICANT: KELLY, ROBERT J
TITLE OF INVENTION: GDP-L-PUCOSE: BETA-D-CALACTOSIDE
TITLE OF INVENTION: 2-ALPHA-L-FUCOSYLITRANSFERASES, DNA SEQUENCES ENCODING THE
TITLE OF INVENTION: GAME, METHOD FOR PRODUCING THE SAME AND A METHOD OF
TITLE OF INVENTION: GENOTYPING A PERSON
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2;
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                                                                                                                                                                                                                                                                                                                                                          AUDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT STRRET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/395,800A
FILING DATE: 28 FEB-1995
FILING DATE: 28 735
                                314 LKLFKPEAAFLPEWIGIEADLSPLLK 339
       301 LKVFKPEAAFLPEWVGIPADLSPLLK 326
                                                                                                                                     Sequence 8, Application US/08395800A
Patent No. 5807732
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TELECOMMUNICATION: TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UF
INFORMATION FOR SEQ ID NO: 8:
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Best Local Similarity 79.1%
Matches 258; Conservative
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                                                                                                                                                                                      APPLICANT: LOWE, JOHN B
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TOPOLOGY:
                                                                                                                    US-08-395-800A-8
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61 GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWONYHLNDWMER 120
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APPLICANT: Eric H. Holmes et al.
TITLE OF INVENTION: NGCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
APPLICANT: SANDEIN, MAURO S.
APPLICANT: SANDEIN, MAURO S.
TITLE OF INVENTION NUCLEIC ACIDS FOR REDUCING CARBOHYDRAIE EPITOPES
FILE REFERENCE: 30562.5050
CURRENT APPLICATION NUMBER: US/09/254,077A
CURRENT FILING DATE: 1999-06-11
PRIOR APPLICATION UNBER: PCT/AU97/00540
PRIOR PELING DATE: 1997-08-22
PRIOR PELING DATE: 1996-08-23
PRIOR PILING DATE: 1996-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 VQQRLAKIQAM--WELPV-----QIPVLASTSKALGPSQLRGWWINAIGRLGNQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LOORIVKLOPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.1%; Score 1386.5; DB 4; 79.1%; Pred. No. 1.2e-151; 1ve 26; Mismatches 31;
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DB 4;
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                                                                                              LKVFKPEAAFLPEWVGIPADLSPLLK 326
                                                                                                               PCT-US91-00899-11; Sequence 11, Application PC/TUS9100899; GENERAL INFORMATION:
                                                                                                                                                                                        Sequence 12, Application US/09254077A Patent No. 6399758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 63.33
Matches 200; Conservative
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                                                                                                                                                                                                  Patent No. 6399758
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Lepus
                                                                                                                                                                          US-09-254-077A-12
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                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 12
LENGTH: 373
                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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                    201
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                                                                                                                                                      61 GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120
                                                                                                                                                                      YRHI-PGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTF 179
                                                                                                                                                                                                                                                                                        256
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                                                                                                                    1 LQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSLGRLGNQM 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: SANDRIN, MAURO S.
APPLICANT: MCKENZIE, IAN C. F.
TITLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
FILE REPRENCE: 30562.505W0
CURRENT APPLICATION NUMBER: US/09/254,077A
                                                                                                                                                                                                                                                          VGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSFVFVVTSNGMAMCRENINA
                                                                                                                                                                                                                                                                          240 SRGDVVFAGNGIĘGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS
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                                                        Length 344;
                                                                                 Indels
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                                                  72.6%; Score 1376; DB 4; I
78.9%; Pred. No. 2e-150;
Live 26; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/AU97/00540 PRIOR FILING DATE: 1997-08-22 PRIOR APPLICATION NUMBER: PO 1823 PRIOR FILING DATE: 1996-08-23
                                                                                                                                                                                                                                                                                                                                                                             300 FLKVFKPEAAFLPEWVGIPADLSPLLK 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application US/09254077A Patent No. 6399758
                                                              Best Local Similarity 78.9
Matches 258; Conservative
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Best Local Similarity 79.1
Matches 258; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1996-(NUMBER OF SEQ ID NOS: 12
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Ver.
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US-09-254-077A-9
                        US-09-298-886-11
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                                                    Query Match
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APPLICANT: Lowe, John B. TITLE OF INVENTION: Method and Products For the Synthesis of TITLE OF INVENTION: Oligosaccharide Structures on Glycoproteins, Glycolipids, TITLE OF INVENTION: or as Free Molecules, and For the Isolation of Cloned TITLE OF INVENTION: Genetic Sequences That Determine These Structur
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RGDVVFAGNGIEGSPAKDFALLTQCNHTIMIIGTFGIWAAYLAGGDTIYLANYTLPDSPF 300
                                      248
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                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SANDRIN, MAURO S.
APPLICANT: SANDRIN, MAURO S.
APPLICANT: SANDRIN, MAURO S.
APPLICANT: MCKENZIE, IAN C. F.
TITLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRAIE EPITOPES
FILE REPERENCE: 3052.55070
CURRENT APPLICATION NUMBER: US/09/254,077A
CURRENT FILING DATE: 1997-06-11
PRIOR FILING DATE: 1997-08-22
PRIOR FILING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN VOR: 2.1
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STREET:
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US-08-393-246-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 GTAMGPNASSSCPQH-PASLSGTWTVYPNGRFGNQMGQYATLLALAQLNGRRAFILPAMH 85
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                       3: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
3: P.C.
1755 Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                 SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/00899
FILING DATE: 19910214
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye Ph.D., Jean-Paul
REGISCRATION NUMBER: 31,451
TELECOMMUNICATION INFORMATION:
MEDICOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 1051.5; DB 5; Pred. No. 6.2e-113; 37; Mismatches 73;
                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                          COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/07914281; Patent No. 5324663
GENERAL INFORMATION: APPLICANT: LOWE, JOHN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.5%;
63.3%;
                                                                                                                                                                                                                                                                                                                   (703)521-5940
                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 333 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                         TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              C-terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 195; Conservative
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              CORRESPONDENCE ADDRESS
NUMBER OF SEQUENCES:
                                                              CITY: Arithy...
STATE: Virginia
7TP: 22202
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HYPOTHETICAL: YES
FRAGMENT
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                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                TELEPHONE:
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                                                       STREET:
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OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS, GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE SIRUCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 GTAMGPNASSSCPQH-PASLSGTWTVYPNGRPGNQMGQXATLLALAQLNGRRAFILDAMH 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 DRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALL 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 365;
        METHODS AND PRODUCTS FOR THE SYNTHESIS
                                                                                                                             OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                          SCEE: P.C.
F: 1755 Jefferson Davis Highway, Fourth Floor
Arlington
                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.58; Score 1051.5; DB 1; 63.3%; Pred. No. 7.2e-113; W.smatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                     ELLING CALL.

CLASSIFICATION: 530
ALTORNEY/AGENT INFORMATION:
NAME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REFERENCE/POCKET NUMBER: 2363-060-55
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/914,281
FILING DATE: 19920720
                                                                                                                                                                                                                                         ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Patent No. 5595900
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 365 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 63.3%
Matches 195; Conservative
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-07-914-281-6
TITLE OF INVENTION: M
TITLE OF INVENTION: G
TITLE OF INVENTION: G
NUMBER OF SEQUENCES:
                                                                                                     CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
                                                                                                                                                                                                              Virginia
                                                                                                                                                                                                                                 U.S.A.
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                                                                                                                           ADDRESSEE:
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PAGES: 6674
DATE: 1990
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   METHODS AND PRODUCTS FOR THE SYNTHESIS OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS, GIYCOLIFIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298 TQCNHTIMTIGIFGFWAAYLAGGDTVXLANFTLPDSEFLKIFKPEAAFLPEWVGINADLS 357
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                                                                                                    OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
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                                                                                                                  s: P.C.
1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.5%; Score 1051.5; DB 1; 63.3%; Pred. No. 7.2e-113; tive 37; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220,433
FILING DATE: 30-MAR-1994
APPLICATION NUMBER: US 07/914,281
FILING DATE: 20-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: LAVAILEY, JGan-Paul N. P.
REGISTRATION NUMBER: 31,451
TRECHENCE/DOCKET NUMBER: 2363-060-55
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                      US/08/393,246
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SE
TITLE OF INVENTION: OF TITLE OF INVENTION: OF TITLE OF INVENTION: OF TITLE OF INVENTION: OF UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530
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                                                                                                                                                   CITY: Arlington
STATE: Virginia
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                                                                                                                    ADDRESSEE:
                                                                                                                                                                                    COUNTRY:
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RESULT 13

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"GDP-L-fucose;beta-D-Galactoside-2-alpha-L-fucosyl
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Sequence 1, Application US/08273411
Patent No. 562524
GENERAL INFORMATION:
GENERAL INFORMATION: Falk, Per
APPLICANT: Gordon, Jeffrey I.
TITLE OF INVENTION: Animal Model for Gastro-Intestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1: FROM 1 TO 365
                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,411
                                                                                                                                                                            3: Patrea L. Pabst
1100 Peachtree Street, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NOBER: 31,284
REFERENCE/DOCKET UNMER: WU10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 815-650
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
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Proc. Nat'l Acad.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 63.3%
Matches 195; Conservative
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                                                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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CLASSIFICATION: 435
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ZIP: 30309-4530
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                                                                                                                                                                                                          CITY: Atlanta
STATE: Georgia
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FRAGMENT TYPE:
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GDP-L-FUCOSE: BETA-D-GALACTOSIDE
2-ALPHA-L-FUCOSYLTRANSFERASES, DNA SEQUENCES ENCODING THE
SAME, METHOD FOR PRODUCING THE SAME AND A METHOD OF
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        TOCNHIIMTIGIFGIWAAYLAGGDIIYLANYTLPDSPFLKVFKPBAAFLPEWVGIPADLS 322
                                 298 IQCNHIINTIGIEGEWAAYLAGGDIVYLANFILPDSEFLKIEKPEAAFLPEWVGINADLS 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
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28-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
                                                                                                                                                                                                                                      Sequence 6, Application US/08395800A patent No. 5807732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                       APPLICANT: ROUQUIER, SYLVIE
APPLICANT: GIORGI, DOMINIQUE
APPLICANT: KELLY, ROBERT J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (703) 413-3000
(703) 413-2220
                                                                                                                                                                                                                                                                                                   APPLICANT: LOWE, JOHN B APPLICANT: LENNON, GREGORY
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amino acid
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INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US
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TITLE OF INVENTION: S
TITLE OF INVENTION: S
TITLE OF INVENTION: G
NUMBER OF SEQUENCES:
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Best Local Similarity
Matches 195; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VIRGINIA
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                                                                                                                                        358 PLWTLAKP 365
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                                                                                                                                                                                                                                                                                                                APPLICANT: LOWE, JOHN B.

TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROPEINS,
TITLE OF INVENTION: GLYCOLIFIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
TITLE OF INVENTION: OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
NUMBER OF SEQUENCES. 23
CORRESPONDENCE ADDRESS:
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238 DSAXIRQAMDWFRARHEAPVFVVTSNGMEWCKENIDTSQGDVTFAGDGQEATPWKDFALL 297
                                                              25 GNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMH 84
                                            263 IQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS
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1755 Jefferson Davis Highway, Fourth Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOPTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILLING CLASSIFICATION: 452 CLASSIFICATION:
ATTORNEY/AGENT INPORMATION:
NAME: Lavalleye, Jean-Paul M. P.
NAME: Lavalleye, 31,451
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                Sequence 6, Application US/08525058A Patent No. 5770420 GENERAL INFORMATION: APPLICANT: LOWE, JOHN B.
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TELEPA: (703)486-2347
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 6
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MEDIUM TYPE: Floppy disk
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Search completed: May 27, 2003, 15:11:52 Job time : 15.5136 secs

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Matches 353;
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SEQ ID NO 10
LENGTH: 353
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Seguence 4,
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                                                                              1 LQORIVKLQPLSEKELPMTT.....RSHFHLKAKGVTCYVAGRAF
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  GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                           - protein search, using sw model
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ALIGNMENTS

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                                 GENERAL INFORMATION:
APPLICANT: Eric H. Holmes et al.
APPLICANT: Eric H. Holmes et al.
TITLE OF INVENTION: MOLLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE
TITLE OF INVENTION: GMI-SPECIFIC ALPHAI-2 FOCOSYLTRANSFERASE AND USES
TITLE OF INVENTION: THEREOF US/09/999,672
CURRENT APPLICATION NUMBER: US/09/999,672
CURRENT FILING DATE: 2001-10-31
PRIOR PELLING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 29
SOFTWARE PLANCE OF NOS: 29
SOFTWARE PALENT OF NOS: 29
SOFTWARE PALENT OF NOS: 29
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100.0%; Pred. No. 3.9e-188;
ive 0; Mismatches 0;
Sequence 10, Application US/0999672
Patent No. US20020127655A1
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PRIOR FILING DATE: 1999-04-26
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US-09-999-672-8
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IITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE
TITLE OF INVENTION: GAL-SPECIFIC ALPHA1-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 8511-029
CURRENT APPLICATION NUMBER: US/09/999,672
CURRENT FILING DATE: 2001-10-310
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     RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF 300
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GENERAL INFORMATION:

APPLICANT: Eric H. Holmes et al.

TITLE OF INVENTION: MGCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE

TITLE OF INVENTION: MGCLEIC ALPHAI-2 FUCOSYLTRANSFERASE AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: 8511-029

CURRENT APPLICATION NUMBER: US/10/040,863

CURRENT FILING DATE: 2001-11-01

PRIOR FILING DATE: 1999-04-23

PRIOR FILING DATE: 1999-04-23
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100.0%; Pred. No. 3.9e-188;
iive 0; Mismatches 0;
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                                                                                                                                                                                                   Sequence 10, Application US/10040863
Patent No. US20020137165A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Rattus norvegicus
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
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Matches 353; Conservative
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51 GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWWEER 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS 240
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Sequence 8, Application US/10040863

Fatent No. US20020137165A1

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A FAT GANGLICSIDE
TITLE OF INVENTION: THEREOF
CURRENT PRILICATION NUMBER: US/10/040,863
CURRENT PILING DATE: 2001-11-01
                                                                                                                                                                                                                                                                                                                           61 GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120
                                                                                                                                                                                                                                                                                                                                                     YRHIPGHFVRFIGYPCSWIFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFV 180
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                                                                                                                                                                                                                                                                 28 LQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTRNSIGRLGNQM 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 LKVFKPEAAFLPEWVGIPADLSPLLKALTPACPRSHFHLKAKGVTCYVAGRAF 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1896; DB 12; Length 380; 100.0%; Pred. No. 4.4e-188;
                                                                                                                                                                                                    6
                                                                                                                                                          Length 380;
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                                                                                                                                                                                                      Indels
                                                                                                                                                            DB 10;
                                                                                                                                                        Score 1896; DB 10;
Pred. No. 4.4e-188;
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                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/298,886
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEATT NOTE: 1999-04-23
                                                                                                                                                            100.0%;
larity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) ORGANISM: Rattus norvegicus US-10-040-863-8
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Best Local Similarity 100.
Matches 353; Conservative
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver.
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Best Local Similarity
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240
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61 GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120
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28 LOQRAVKIQP--TWELDMVIQVT---TESP-----SSPQLKGWWTINAIGRIGNQM 73
                                                                                           241 RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPBSPF
                                                         GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS
                                                                                                                                                                                                                                                                                 APPLICANT: MCERZIE, IAN FAROUHAR CAMPBELL
APPLICANT: SANDRIN, MAURO SERGIO
ITILE OF INVENITION: IMPROVED NUCLEIC ACIDS ENCODING A CHIMERIC
ITILE OF INVENITION: GLYCOSYLIRANSFERASE
FILE REFERENCE: 30562.60SNO
CURRENT APPLICATION NUMBER: US/09/051,034A
CURRENT FILING DATE: 1998-03-31
PRIOR FILING DATE: 1997-08-01
PRIOR FILING DATE: 1997-08-01
PRIOR FILING DATE: 1996-08-21
PRIOR FILING DATE: 1996-08-21
PRIOR FILING DATE: 1996-08-21
PRIOR FILING DATE: 1996-08-01
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                                                                                                                                                  LKVFKPEAAFLPEWVGIPADLSPLLKALTPACPRSHFHLKAKGVTCYVAGRAF 353
                                                                                                                                                                  75.4%; Score 1430; DB 10; Length 340; 81.9%; Pred. No. 7.7e-140;
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                                                                                                                                                                                                                                               Sequence 2, Application US/09051034A
Patent No. US20010055584A1
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                                                                                                                                                                                                                                                                         GENERAL INFORMATION
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US-09-051-034A-2
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Best Local S
              148
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RESULT 6 US-09-999-672-11

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GENERAL INFORMATION:

APPLICANT: Eric H. Holmes et al.

APPLICANT: Eric H. Holmes et al.

TITLE OF INVENTION: GML-SPECIFIC ALPHAI-2 FUCOSILTRANSFERASE AND USES

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: GML-SPECIFIC ALPHAI-2 FUCOSILTRANSFERASE AND USES

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: GML-SPECIFIC ALPHAI-2 FUCOSILTRANSFERASE AND USES

TITLE OF INVENTION: THEREOF

CURRENT APPLICATION NUMBER: US/09/999,672

CURRENT FILING DATE: 2001-10-31

PRIOR FILING DATE: 1999-04-26

NUMBER OF SEQ ID NOS: 29

SOFTWARF PRILING VALUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 YRHI-PGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTF 179
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| Sequence 11, Application US/10040863
| Patent No. US20020137165A1
| Patent No. US20020137165A1
| APPLICANT: Eric H. Holmes et al. APPLICANT: Eric H. Holmes et al. APPLICANT: Eric G. Holmes et al. TITLE D'E INVENTION: UGULEIC ACIDS AND PROTEINS OF A RAT GANGLICSIDE
| TITLE D'E INVENTION: UGUL-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERASE AND USES
| TITLE OF INVENTION: THEREOF
| FILE REPERBENCE: 8511-029
| FURRENT APPLICATION NUMBER: US/10/040,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1376; DB 12; Length 344; Pred. No. 3.1e-134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.6%; Score 1376; DB 10; 78.9%; Pred. No. 3.1e-134; ative 26; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLKVFKPEAAFLPEWVGIPADLSPLLK 326
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PRIOR APPLICATION NUMBER: 09/298,886
PRIOR FILING DATE: 1999-04-03
Sequence 11, Application US/09999672 Patent No. US20020127655A1
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78.98;
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SEQ ID NO 11
LENGTH: 344
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                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
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Best Local Similarity
Matches 258; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 344
TYPE: PRT
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us-10-040-863-10.rapb

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OF OLIGOSACCHARIDE STRUCTURES ON GIXCOPROTEINS, GLYCOLIFIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
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        298 IQCNHIIMIIGIFGFWAAYLAGGDTVYLANFTLPDSBFLKIFKPEAAFLPEWVGINADLS 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 GNTESPEMREDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMH 84
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                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
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                                                                                                                                                                                                                                                                       APPLICANT: LOWE, JOHN B.
TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.5%; Score 1051,5; DB 10
llarity 63.3%; Pred. No. 1.5e-100;
Conservative 37; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 2363-060-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/863,475A FILING DATE: 24-May-2001
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APPLICATION NUMBER: 07/914,281
FILING DATE: 20-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNET/AGENT INFORMATION:
NAME: Lavalleye, Jean-Paul M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown;
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: US-09-863-475A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 31,451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
                                                                                                                                                                                                         US/09863475A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 365 amino acids
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TELEX: 248855 OPAT UR
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                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 14 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 22202
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
                                                                                                                                                                                                       Sequence 6, Application US, Patent No. US20020102688A1 GENERAL INFORMATION:
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Matches 195; Conserv
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                                                                                                  358 PLWTLAKP 365
                                                            323 PLLKALTP
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                                                                                                                                                                   RESULT 9
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APPLICANT: Denning, Chris
APPLICANT: Denning, Chris
APPLICANT: Denning, Chris
APPLICANT: Clark, A. John
APPLICANT: Clark, J. Michael
TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Compatible for Human
TITLE OF INVENTION: Transplantation and a Carbohydrate Determinant Selection System
TITLE OF INVENTION: Recombination
FILE REFERENCE: 731/02
CURRENT APPLICATION NUMBER: US/10/105,963
CURRENT FILING DATE: 2002-03-21
PRIOR FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                           VGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINA 239
                                                                                                                          61 GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120
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                                                                       28 VQQRLAKIQAM--WELPV------QIPVLASISKALGPSQLRGMWIINAIGRLGNQM 76
  Gaps
                                        LQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM 60
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  Indels
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31;
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    Mismatches
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    26;
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SEQ ID NO 10
LENGTH: 365
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Matches 195; Conservative
  Conservative
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    258;
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TITLE OF INVENTION: METHODS AND COMPOSITIONS TO IDENTIFY SWINE GENETICALLY TITLE OF INVENTION: RESISTANT TO F18 E. COLI ASSOCIATED DISEASES FILE REPRENCE: 2149/9/086 E. COLI ASSOCIATED DISEASES CURRENT APPLICATION NUMBER: US/09/844,268 PRIOR APPLICATION NUMBER: 09/443,766 PRIOR PILING DATE: 1999-11-19 NUMBER OF SEQ. ID NOS: 13
SOFTWARE: PATENTING DATE: 1999-11-19
NUMBER OF SEQ. ID NOS: 13
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TITLE OF INVENTION: METHODS AND COMPOSITIONS TO IDENTIFY SWINE GENETICALLY
TITLE OF INVENTION: RESISTANT TO F18 E. COLI ASSOCIATED DISEASES
TITLE OF INVENTION: RESISTANT TO F18 E. COLI ASSOCIATED DISEASES
CURRENT APPLICATION NUMBER: US/09/844,705
CURRENT FILING DATE: 2001-04-27
PRIOR PILING DATE: 199-11-19
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PACHULIN Ver. 2.0
SEQ ID NO 13
LENGTH: 365
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62.6%; Pred. No. 8e-100;
Live 38; Mismatches 75; Indels
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Patent No. US20020138836A1
GENERAL INFORMATION:
APPLICANT: BOSWORTH, BRAD
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Best Local Similarity 62.6%;
Matches 194; Conservative
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Matches 194; Conserv
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                                                                      263 TQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLS
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APPLICANT: MCKENZIE, IAN FARQUHAR CAMPBELL
APPLICANT: SANDRIN, MATRO SERGIO
ATTLE OF INVENTION: IMPROVED NUCLEIC ACIDS ENCODING A CHIMERIC
TITLE OF INVENTION: GIYCOSYTRANSFERASE
FILE REFERENCE: 30562.605WO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/051,034A
CURRENT APPLICATION NUMBER: US/09/051,034A
CURRENT APPLICATION NUMBER: US/09/051,034A
PRIOR PILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: PCT/AU97/00492
PRIOR PILING DATE: 1997-08-01
PRIOR PILING DATE: 1996-08-21
PRIOR FILING DATE: 1996-08-21
PRIOR FILING DATE: 1996-08-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin VO-
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Sequence 13, Application US/09844268
Sequence 10, US20020129395A1
SEBERAL INFORMATION:
APPLICANT: BOSWORTH, BRAD
                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09051034A Patent No. US20010055584A1
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Matches 194; Conservative
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Sequence 14, Application US/09479614

Publication No. US20030013183A1

GENERAL INFORMATION:
APPLICANT: McCall, Catherine
APPLICANT: Weber, Enic
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
FILE REFERENCE: P-1047
CURRENT APPLICATION NUMBER: US/09/479,614
CURRENT APPLICATION NUMBER: 60/115,033
EARLIER PILING DATE: 1999-01-07
SEALIER PILING DATE: 1999-01-07
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                   APPLICANT: Yang, Yong-Min APPLICANT: Barankiewicz, Theresa J. APPLICANT: Barankiewicz, Theresa J. APPLICANT: Chen, Zhong TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREPERENCE: IGE-00101.P.1.1 CURRENT APPLICATION NUMBER: US/10/214,524 CURRENT FILING DATE: 2002-08-08 PRIOR FILING DATE: 2002-08-08 PRIOR FILING DATE: 2001-08-08 PRIOR FILING DATE: 2001-08-13 PRIOR FILING DATE: 2001-08-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 GHFVRFTGYPCSWTFYHHLRPBILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFVGVHVR 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 VVFAGNGIEGSPAKDFALLFQCNHTIMIGTFGIWAAYLAGGDTIYLANYTLPDSP---F 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.2%; Score 99; DB 9; Length 496; llarity 25.0%; Pred. No. 0.14; Conservative 21; Mismatches 84; Indels
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                                                                                                                         Sequence 25, Application US/10214524 Publication No. US20030073142A1 GENERAL INFORMATION:
                                                                                                                                                                                                 APPLICANT: Chen, Swey-Shen Alex
                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Cat (Felis catus) US-10-214-524-25
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Best Local Similarity
Matches 55; Conserv
     HENILCKEWVKI --
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US-09-479-614-14
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US-09-479-614-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 GIDYQKKALEYMAKRVPNMELFV-----FCE------DIKFTQNLDLGYPFTDMTTR 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261 -----LITQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPD----SPFLKVFK 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 DKEEEAXWDMLLMQSCKHGIIANSTYSWWAAYL-----MEN---PEKIIIGPKHWLFG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 FILPPPPENNKNNKKEEEEYQRKLS--LILAAKNSVF--VHIRRGDYVGI-----GCQL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152 FIL------HDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA 202
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                                                                                                                                                                                                                                                                                                                                                           PAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEW 314
                                                                                                                                                                                                                                                                                                                                                                                          51 PVAIFCLAGTPVHPNASDSCPKH-PASFSGTWIIYPDGRFGNQMGQYATLLALAQLNGRQ 109
                                                                                                 195 NVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAMCRENINASRGDVVFAGNGIEGS
                                                                                                                                                               137 SWIFYHHLRPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMP
                                                                77 AFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFIGYPC
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GENERAL INC. COLOURS.
APPLICANT: Taylor, Diane
APPLICANT: Wang, Ge
TITLE OF INVENTION: ALPHA 1,2-FUCOSYLTRANSFERASE
TITLE OF INVENTION: ALPHA 1,2-FUCOSYLTRANSFERASE
FILE REFERENCE: 07254-061002
CURRENT APPLICATION NUMBER: US/09/848,838
CURRENT APPLICATION NUMBER: US 09/433,598
PRIOR APPLICATION NUMBER: US 09/433,598
PRIOR FILING DATE: 1999-11-02
PRIOR FILING DATE: 1999-11-02
PRIOR FILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 23
SOSTWARE: FASLSEQ for Windows Version 4.0
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24.0%; Pred. No. 2.9e-06;
cive 33; Mismatches 125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09848838
Patent No. US20020037570A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT; ORGANISM: Helicobacter pyloriUS-09-848-838-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 24.0%
Matches 81; Conservative
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244 VVFAGNGIEGSPAKDFALLIQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSP---F 300
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Search completed: May 27, 2003, 15:25:43 Job time : 16.2516 secs

GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

using sw model OM protein - protein search,

on:

May 27, 2003, 15:00:45 ; Search time 12.7916 Seconds (without alignments) 2652.940 Million ceil updates/sec

US-10-040-863-10 1896 1 LOCRIVKLQPLSEKELPMTT.....RSHFHLKAKGVICYVAGRAF Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283224 segs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 20000000000 Minimum DB : Maximum DB :

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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C; Species: Homo sapiens (man)
C; Accession: A56098
R; Kelly, R.U.; Rouquier, S.; Giorgi, D.; Lennon, G.G.; Lowe, J.B.
B; Chem. Comen. 270, 4640-4649, 1995
A; Title: Sequence and expression of a candidate for the human Secretor blood group all A; Reference number: A56098; MUID:95181460; PMID:7876235
A; Reference number: A56098; MUID:95181460; PMID:7876235
A; Accession: A56098
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-343 < KEL>
A; Cross-references: GB:U7894; NID:9687618; PIDN:AAC24453.1; PID:9687619
A; Gneetics:
A; Gneetics:
A; Cross-references: GB:U7894; NID:182100
A; Cross-references: GB:U7894; NID:182100
A; Map Position: 19913-3-19913.3
C; Keywords: glycoprotein; Golgi apparatus; transmembrane protein 2, GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120 180 196 Gaps 1 LOORIVKLOPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM 60 YRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFV GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS 241 RGDYVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF Query Match
Dest Local Similarity 79.1%; Pred. No. 1.3e-108;
Matches 258; Conservative 26; Mismatches 31; Indels 11; LKVFKPEAAFLPEWVGIPADLSPLLK 326 61 121 181 301 δğ QQ QΣ PP á g $\dot{\Omega}$ Dp δ qq Óγ

RESULT 2

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ogalactoside 2-alpha-L-fucosyltransferase (BC 2.4.1.69) B - rat (fragment)
Myllernate names: alpha-1.2-fucosyltransferase
C;Species: Rattus norvegicus (Norway rat)
C;Becies: Rattus norvegicus (Norway rat)
C;Becies: 26-Dec-1994 #sequence_revision 23-Peb-1996 #text_change 08-Oct-1999
C;Baccession: S46494
R;Piau, J.P.; Labarriere, N.; Dabouis, G.; Denis, M.G.
Blochem. J. 300, 623-626, 1994
A;Title: Evidence for two distinct alpha-(1,2)-fucosyltransferase genes differentiall
A;Reference number: S46493; MUID:94280382; PMID:8010942
A;Accession: S46494
A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 NALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 RPEILKEFTLHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMPNVWKGVVA 202
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                                             A;Molecule type: mRNA
A;Residues: 1-365 <LAR>
A;Cross-references: GB:M35531; NID:9183887; PID:9306830
C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 365;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Larsen, R.D.; Ernst, L.K.; Nair, R.P.; Lowe, J.B. Proc. Natl. Acad. Sci. U.S.A. 87, 6674-6678, 1990
A; Title: Molecular cloning, sequence, and expression of A; Reference number: A36047; MUID:90370848; PMID:2118655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.5%; Score 1051.5; DB :
63.3%; Pred. No. 1.8e-80;
tive 37; Mismatches 73
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344 AFLPEWVGINADLSPV 359
                                                                                                                                                                                                                                                                                  309 AFLPEWVGIPADLSPL 324
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Best Local Similarity
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                                                                                                                                                     R;Hitoshi, S.; Kusunoki, S.; Kanazawa, I.; Tsuji, S.
J. Biol. Chem. 270, 8844-8850, 1995
A;Title: Molecular cloning and expression of two types of rabbit beta-galactoside alphal
A;Reference number: A56392; MUID:95238380; PMID:7721792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of rabbit beta-galactoside alpha
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beta-galactoside alphal, 2-fucosyltransferase I - rabbit
c; Species: Oryctolagus cuniculus (domestic rabbit)
c; Date: 19-oct-1995 #sequence_revision 19-oct-1995 #text_change 05-Nov-1999
C; Accession: A56392
R; Hitcoshi, S.; Kusunoki, S.; Kanazawa, I.; Tsuji, S.
R; Hitcoshi, S.; Kusunoki, S.; Kanazawa, I.; Tsuji, S.
A; Title: Molecular cloning and expression of two types of rabbit beta-galact
A; Reference number: A56392; MUID:95238380; PMID:7721792
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 05-Nov-1999
C;Accession: B56392
R;Hitoshi, S.; Kusunoki, S.; Kanazawa, I.; Tsuji, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPMTTQMS-----SGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 IPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAF 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 LRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVV 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross_references: GB:X80225; NID:g854356; PIDN:CAA56512.1; PID:g854357
C;Keywords: transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.1%; Score 1291; DB 2; Length 3 83.9%; Pred. No. 1.4e-100; iive 20; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44; Mismatches
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Matches 200; Conservative
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Matches 235; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-354 <HIT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
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Accession: H87911

Ranonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

Science 282, 2012-2018, 1998

ATILLE: Genome sequence of the nematode C. elegans: a platform for investigating bio A:Reference number: A75000; MUID:99069613; PMID:9851916

A:Note: see websites genome wustl.edu/gsc/C_elegans/ and www_sanger ac.uk/Projects/C A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A:Accession: H87911

A:Status: pre-liminary

A:Rolecule type: DNA

A:Residues: 1-443 csTO>

A:Cross-references: GB:chr_I: PIDN:AAC16988.1; PID:93150470; GSPDB:GN00019; CESP:B020

A:Note: contains weak similarity to fucosyltransferases
C;Genetics:
A:Genetics:
A
   A;Title: The genes responsible for O-antigen synthesis of Vibrio cholerae 0139 are A;Reference number: Z22749; MUID:99453293; PMID:10521656
                                                               A. Scession: T4428
A. Status: preliminary; translated from GB/EMBL/DDBJ
A. Molecule type: DNA
A. Molecule type: DNA
A. Residues: 1-281 - (AMA)
A. Cross-references: EMBL:AB012957; NID:q4115688; PIDN:BAA33632.1; PID:q3721682
C. Genetics: A. Note: wbla
C. Superfamily: Vibrio cholerae hypothetical protein wbla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein B0205.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May_2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---NDWMEERYRHI-----PGHFVRFT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GYPCSWIFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 MPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIE 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 HPEIG----VLDIDYYKRAVDXIKEKIEAPVFFVFSNDVAWCKDNFNFIDSPVFIEDTQTE 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 MFTINSIGRLGNQMGEYATLFALARMNG---RL---AFIPASMHNALAPIFRISLPVLHS 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 IGNLMFQVAGLLSIARETGSILLIPSTTTLRRAFDFETTFNDSIOFVGEDLSROLAEDLN 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 ------PWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKE-FTLH 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASKITLTSCCAYRNLSTILFNDSRI-----IERIDGYFQNFRWÄHPDSOKIVKKLFTFM 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253 GSPAKDFALLTQCNHTIMTIGTFGIWAAYL-AGGDTIYLANYT------LPDS 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---IDDLMLMCQCQHNIVANSSFSWWAAWLNSNVDKIVIAPKTWMAENPKGYKWVPDS 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 DIANED--EIFHLKGSSNRLSRILRRLGWLKKNTYYAEKORTIYDVSVFMOAPRY---LD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 281;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.3%; Score 214.5; DB 2; 26.5%; Pred. No. 2e-10; live 50; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.7%; Score 183; DB 2; L/
20.6%; Pred. No. 1.6e-07;
tive 53; Mismatches 128;
Title: The genes responsible for O-antigen
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Best Local Similarity 20.65
Matches 72; Conservative
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Matches 79; Conserv
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C;Species: Vibrio cholerae
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 28-Jul-2000
C;Accession: T44328
R;Yamasaki, S.; Shimizu, T.; Hoshino, K.; Ho, S.T.; Shimada, T.; Nair, G.B.; Takeda, Y.
Gene 237, 321-332, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A: Molecule type: mRNA
A: Residues: 1-142 <PIA>
A: Residues: 1-142 <PIA>
A: Cross-references: EMBL-
B: Chom. J. 300, 623-626, 1994
A: Title: Evidence for two distinct alpha-(1,2)-fucosyltransferase genes differentially
A: Reference number: $46493; MUID:94280382; PMID:8010942
                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G;Species: Rattus norvegicus (Norway rat)
C;Jate: 07-May-1995 #sequence_revision 17-Nov-1995 #text_change 08-oct-1999
C;Jatession: S51582; S4649;
R;Piau, J.P.; Labbariace, N.; Dabouis, G.; Denis, M.G.
Submitted to the EMBL Data Library, November 1993
A;Reference number: S51582
A;Accession: S51582
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 PAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIXLANYTLPDSPFLKVFKPEAAFLPEW 120
                       A.Cross-references: EMBL:L26010; NID:g414816; PIDN:AAB41515.1; PID:g414817 C;Genetics: A;Gene: FTB C:Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEW 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 PCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVN~-GSQPSTFVGVHVRRGDYVHV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIE 252
                                                                                                                                                                                                                                                                                                                                                                                195 NVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGS 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDGVFAGNGIEGS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 30.6%; Score 581; DB 2; Length 142; Best Local Similarity 73.2%; Pred. No. 1.5e-41; Matches 104; Conservative 15; Mismatches 21; Indels
                                                                                                                                                                                                                         Length 159
                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      galactoside 2-alpha-L-fucosyltransferase (EC 2.4.1.69) - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                315 VGIPADLSPLLKALTPACPRSHFHLKAKGVTCYVAGRAF 353
                                                                                                                                                                                                                         Score 846; DB 2;
Pred. No. 1.1e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       %) Status: preliminary
A; Molecule type: mRNA
Residues: 9-132 <P12>
A; Cross-references: EMBL:L26009
C; Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSPAKDFALLTQCNHTIMTIGT 274
                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.4%;
Matches 158; Conservative
A; Residues: 1-159 <PIA>
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11;

Gaps

193

δ

Qγ QQ 61

g

253

δŏ

121

QQ

RESULT 7 T44328 15;

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A,Description: The sequence of C. elegans cosmid C17A2. A,Reference number: 221098 A,Accession: T31916 53; Conservative Similarity A; Gene: CESP: K06H6.6 A; Gene: CESP:C17A2.4 63; Query Match Best Local S Matches 63 Genetics C; Genetics RESULT 11 d δy QΥ 염 ŏ q δŏ Q ŏ g ŏ g 17; A;Molecule type: DNA A;Residules: 1-363 <WILD. A;Coss-references: EMBL:292830; PIDN:CAB07352.1; GSPDB:GN00023; CESP:F11A5.5 A;Experimental source: clone F11A5 hypothetical protein C17A2.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jul-2000 C;Accession: T19196 R;Sammons, L.; Wohldmann, P. submitted to the EMBL Data Library, July 1997 hypothetical protein F11A5.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000 236 252 278 52 SIGRLGNQMGEYATLFALARMNGRLA--FIPASMR-----NALAPIFRISLPVLHSDT 102 -----LNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEF 152 253 GSPAKDFALL-TQCNHTIMTI--GTFGIWAAYLAGGDTIYLANYTLPDSPFLK----- 302 276 211 138 PSSVKRVKFHQKCCTFDDPSLLDNYEDEYLHLTG-----THYQ-SWKYFSHMRNELI---279 NSPADDLLYAKSNCDVVLITAAHSTFGWWGYFSKGNRVY---YT---DIQFTKDWILETG 153 ILHDHVREEAQAFLRGLRVNGSQPSTFVG-VHVRRGDYVHVMPNVWKGV-VADRGYLEKA 189 ---GYLKTTENTY----MDLPKSGENTFITCVHVRRGDFLRV-----GFHVADENFIRSS 237 LNLISRQVAKRANTAT------VFFGDDYEFMDSLRNRTSKINAFVSQ 217 DPVRKRVSFWNIIYWNIHPTNHRKKPEKSTVSIFSFVTFQLRVDEFLENVGISLTVRNAR 171 V-----NGSQ-----PSTFVGVHVRRGDYVHV--MPNVWKGVVADRGYLEKAL 212 DMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMT 277 VIETNVANDDQALELPEEDAFAKTMMVGVHIRHGMDISMNSRNRIHGHVDTPIEYYKRAI A;Map position: 5 A;Introns: 42/1; 55/2; 136/3; 175/3; 210/2; 243/1; 299/1; 330/3 C;Superfamily: Caenorhabditis elegans hypothetical protein C14C6.3 DB 2; Length 363; 211 IDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIE------IGTFGIWAAYL---AGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGI 317 TGTFGWWSAYLNVNASPDVYYYKHWPAPGSVMEKMTNKTEYFLKSWTAL 442 9.0%; Score 170.5; DB 2; Length 23.4%; Pred. No. 1.4e-06; tive 45; Mismatches 101; Indels Rigardner, A. submitted to the EMBL Data Library, March 1997 submitted to the EMBL Data Library, March 1997 A; Reference number: 219319 A; Accession: 720745 A; Accession: 720745 A; Status: preliminary; translated from GB/EMBL/DDBJ Conservative FEISEDYYLPHW 345 303 VFKPEAAFLPEW 314 Best Local Similarity Matches 73; Conserv 103 AKKIPWQNYH---CESP:F11A5.5

Query Match

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C; Genetics:

C; Accession: T20745

272 394

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RESULT 9

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A,Cross-references: EMBL:AF024500; PIDN:AAB70365.1; GSPDB:GN00023; CESP:K06H6. A,Experimental source: strain Bristol N2; clone K06H6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 5
A;Introns: 17/1; 32/2; 58/1; 111/3; 150/3; 184/2; 218/1; 243/3; 272/1; 303/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C14C6.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000
C;Accession: T32294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMHNALAPIFRISLP-----DWMEER 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 PKSIKOTPFOKVCCRHENPELLEKIDEKYLHLTGMFYQ-----SWKYFPNMREQLL--- 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 ---DFLDDSSQDF--GNLPRSNQRTHVTCVHARRGDFVDV-----GFQAADPDFIRNSV 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 AKKI---PWQ-----NYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEF 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153 TLHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGV-VADRGYLEKAL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 SIGRLGNQMGEYATLFALARMNGR--LAFIPASMHNALAPIFRISLP------VLHSDT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196 KYIAENFIPEIEYKKVHRKVVIFGDDLEFMRSLFENSVVSTDEPEYMFPAEYYISQNSPA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 SGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLA--FIPA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 DMFRARYSSPV-----FVVTSNGMAWCR---EN--INASRGDVVFAGNGI--EGSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93;
                                                                                                                                                                                                                            A,Map position: 2
A,Introns: 94/3; 133/3; 168/2; 272/1
C,Superfamily: Caenorhabditis elegans hypothetical protein C14C6.
                                                                                                                                                                                                                                                                                                                                                           8.1%; Score 154; DB 2; Length 348; 22.8%; Pred. No. 3.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 22.8%; Pred. No. 3.3e-vo;
Matches 77; Conservative 50; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;David, M.; Wohldmann, P.; Bauer, C.; Clarke, K. submitted to the EMBL Data Library, September 1997 A;Description: The sequence of C. elegans cosmid K06H6. A;Reference number: 221147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein K06H6.6 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Accession: T32294
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-335 < DAV>
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257 KDFALLTQ-CNHTIMTI--GTFGIWAAYLAGGDTIY 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 EDLIYSKONCDIVLISAPKSTEGWWIGYFSKGNKVF 291
                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ΩĎ
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RESULT 10 T31916

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hypothetical p C;Species: Cae C;Date: 15-Oct C;Accession: T K;White, S. submitted to t A;Reference nu A;Accession: T A;Status: prel A;Molecule typ A;Residues: 1- A;Cross-refere A;Cross-refere A;Gene: CESP: R A;Gene: CESP: R A;Gene: CESP: R A;Gene: CESP: R A;Gene: CESP: R A;Gene: CESP: R	Query Match Best Local S Matches 74 Qy 47 MFTI Qy 931 Qy 931 Qy 931 Qy 142 HHLB Qy 142 HHLB Qy 142 HHLB Qy 198 KGW Qy 258 DFM Qy 258 DFM Qy 258 DFM Qy 259 PFL Db 204AC Qy 259 PFL Db 309 VQLC C;Species: Help RESULT 14 H712 E Genor A;Nariecy: str C;Date: 12-Pel C;Date: 12-Pel C;Date: 12-Pel C;Date: 12-Pel C;Date: 12-Pel C;Date: 12-Pel A;Reference n A;Reference n A;Residues: pre- A;Nolecule ty A;Residues: pre- A;Nolecule ty A;Residues: pre- A;Nolecule ty A;Residues: pre- A;Nolecule ty A;Residues: pre- A;Reperimenta C;Genetics: A;Gross refere A;Groes refere A;Groes refere C;Genetics: C;Genetics: A;Groes refere A;Groes
OY 121 YRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQP 176	REBULT 12 Hypothelical protein F08A8.5 - Caenorhabditis elegans Cispecies: Caenorhabditis elegans Alegans Cispecies: Caenorhabditis elegans Alegans Alegans

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Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D. Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F. 176-180, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   omic sequence comparison of two unrelated isolates of the human gastric p
number: A71800; MUID:99120557; PMID:9923682
H71976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rences: GB:AE001447, GB:AE001439, NID:g4154583, PIDN:AAD05659.1, PID:g415
al source: strain J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
                                                                                                                                                                                                                                                                               ences: EMBL: 281537; PIDN: CAB04377.1; GSPDB:GN00019; CESP: F41D3.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ha(1,2)fucosyltransferase - Helicobacter pylori (strain J99)
elicobacter pylori
train J99
eb.1999 #sequence_revision 12-Feb-1999 #text_change 28-Jul-2000
H71976
protein F41D3.6 - Caenorhabditis elegans
venorhabditis elegans
tt-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
T22068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISLPVLHSDTAK------KIPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFY 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYV----HVMPNVW 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VADRGYLEKALDMERARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAK 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALL------TQCNHTIMTI--GTFGIWAAYLAGGDT-IYLANY-TLPDS 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /1; 59/1; 112/3; 150/3; 222/1; 278/1; 308/3; 326/3; 421/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 7.0%; Score 133.5; DB 2; Length 299; Similarity 22.9%; Pred. No. 0.0014; 76; Conservative 38; Mismatches 129; Indels 89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INSIGRLGNOMGEYATLFALARMNGRLAFIPASMHNALAPIFR----
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                                                                                                                                                                                                                liminary, translated from GB/EMBL/DDBJ
pe: DNA
-500 <WLL>
                                                                                                                                     the EMBL Data Library, November 1996 umber: 219508 T22068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :: | | : | |
LOMTK-EDFYPPTW 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KVFKPEAAFLPEW 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ype: DNA
1-299 <ARN>
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13;
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A;Map position: 5
A:Introns: 50/1; 80/2; 140/3; 179/3; 218/2; 253/1; 278/1; 306/3; 325/1; 342/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C14C6.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.Residues: 1-365 <WIL>
A.Cross-references: EMBL: Z81132; PIDN: CAB03434.1; GSPDB: GN00023; CESP: T26E4.4
A: Experimental source: clone T26E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein T26E4.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
C;Accession: T25309
                                                                                                                                                                                                                                                      70 QHLPKLVRDALKYMGFDRVSQEIVFEYEPKLLKPSRLTYFYGYFQDPRYFDAISSLIKQT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                   -----LLTQCNHTIMTIGTFGIWAAYLAG--GDTIYLANYTLPDSPFLKVFKPEAAF 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228 EEAYWDMLLMQSCKHGIIANSTYSWWAAYLINNPGKIII------GPKHWLFGHENIL 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NY -- HINDWME ------ BRYRHIPGHFVRFTGYPCSWTFYHLRPEILKEFT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDY-----VHVMPNVWKGVVADRGYLEK 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197 PSKMAKLAAETVL----TSELKEDLIICTHIRRGDFQTDGVH-QP-----SDPNFTRA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----- NASR 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 ATDFLVKHYOKWHYRTTVVVFGNDVNFSKAVFEDRVSNSSVIPNRTTPPLNFPIPENSPK 304
                                                                                                       --LPVLHSDTAKKIPWQNYHLNDWMEERYRHI-PGHFVRFTGYPCSWTFYHHLRPEILKE 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 GNQMGEYATLFALARMNGRLAFIPA ... ----SMHNALAPIFRISLPVLHSDTAKKIPWQ 109
                                                10 GGLGNQMFQYAFAKSLQKHSNTPVLLDITSFDGSNRKMQLELFPIDLPYASAKEIAIAKM 69
152 FTL----HDHVREEAQAFIRGIR-VNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRG
                                                                                                                                                                                                                                                                                                                           206 YLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFA----
                                                                                                                                                                                                                                                                                                                                                           84;
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6.9%; Score 131; DB 2; Length 365;
Best Local Similarity 20.7%; Pred. No. 0.0028;
Matches 61; Conservative 43; Mismatches 106; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: 220013
A;Accession: T25309
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;McMurray, A.
submitted to the EMBL Data Library, October 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPEWVGIPADLSPLLKALTPACPRSHFHLKAK 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----ESHFEVKSQ 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   280 CKEWVKI--
                                                                                                                                                                                                                                                                                                                                                                            182
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Search completed: May 27, 2003, 15:08:18 Job time : 13.7916 secs

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GenCore version 5.1.4_p5_4578

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2003, 14:53:11; Search time 10.3317 Seconds
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Run on: May 27, 2003, 14:53:11; Search time 10.3317 Seconds (without alignments) 1417.108 Million cell updates/sec Title: US-10-040-863-10 Perfect score: 1896 Sequence: LQQRIVKLQPLSEKELPMTT.....RSHFHLKAKGVTCYVAGRAF 353

Sequence: 1 LQQRIVKLQPLSEKELPMTT....
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: Minimum DB sed length: 0

112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

tion	2 sus servo- 3 bos tauri 1 h galacti 3 mus musc 0 mus musc 0 mus musc 0 poryctola 9 oryctola 6 homo sap 4 rattus n 7 rattus n 7 rattus n 8 phaneroc 8 phaneroc 8 phaneroc 9 partus n 7 rattus n 7 rattus n 8 phaneroc 9 partus n 9 cquine h 10 mus musc 11 mus musc 12 thermus 13 rattus 14 homo sap 14 homo sap 15 mquo sap 16 homo sap 18 rattus 19 rattus 10 homo sap 11 rattus 11 rattus 12 reconnes 13 rattus 14 rattus 15 rattus 16 rattus 17 rattus 18 rattus 18 rattus 19 rattus 19 rattus 10
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DB	:
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Q61409 mus musculu	P76464 escherichia	P45784 vibrio chol	P72933 synechocyst	F87503 human adeno	P97846 rattus norv	P78357 homo sapien	P87379 xenopus lae	Q9z140 helicobacte	P23739 rattus norv		O54991 mus musculu
CN3B_MOUSE	YFAS_ECOLI	GSPN_VIBCH	GLO2_SYNY3	DPOL_ADE04	CTA1_RAT	CTA1_HUMAN	GRB2_XENLA	RIBB_HELPJ	SUIS_RAT	Y285_MYCGE	CTA1_MOUSE
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799	1534	252	257	1193	1381	1384	217	344	1840	347	1385
4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.3	4.3	4.3	4.3	4.3
83.5	83.5	83	82.5	82.5	82.5	82.5	82	82	82	81.5	81.5
34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

us-10-040-863-10.rsp

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30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 2 (EC 2-4.1.69) (GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase 2) (Alpha(1,2)FT 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP + alpha-L-fucosyl-1,2-beta-D-galactosyl-R. PATHWAY: Glycosylation of the substance of the substanc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 LQQRMVKIQP--TWELQMVTQVT---TESP-----SSPQLKGMWTINAIGRLGNQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 YRHIPGHEVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 GVHVRRGDYVHYMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 GVHVRRGDYVHVMPNVWKGVVADRRYLEQALDWFRARYRSPVFVVSSNGMAWCRENINAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                               LUMENAL, CATALYTIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

R -> H (IN REF. 3).
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                                                           EMBL, AF027304; AAC09170.1; -.
EMBL, X99621; CAA67932.1; -.
InterPro; IPR002516; GT_11.
Pfam, PF01531; GJyco_transf_11; 1.
Transferase: Glycosyltransferase; Glycoprotein; Transmembrane; Golgi stack; Signal anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0629F1C04FC206AD CRC64;
                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.5e-113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75.4%; Score 1430; DB 1;
81.9%; Pred. No. 1.5e-113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 1.56
26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38987
                               EMBL; U70881; AAB81883.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267; Conservative
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185
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340 AA;
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Q28113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Petit J.M.;
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CARBOHYD
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CONFLICT
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Matches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last amondation update)
16-JUN-2003 (Rel. 41, Last amondation update)
16-JUN-2004 (Rel. 41, Last amondation update)
16-galactoside 2-L-fucosyltransferase 2 (EC 2.4.1.69) (GDP-L-fucose:beta-
17-galactoside 2-alpha-L-fucosyltransferase 2) (Alpha(1,2)FT 2)
17-galactoside 2-alpha-L-fucosyltransferase) (Secretor factor) (Se) (SE2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                        LQQRIVKLQPLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQM 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 LHQRLEKMQPTWELEA-----LEPATMETPSRPQPRPQLKGWWTINAIGRLGNQM 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                         (FOLDMENAL, CATALYTIC (POTENTIAL).

N-LINKED (GLCNAC, ...) (POTENTIAL).

N-LINKED (GLCNAC, ...) (POTENTIAL).

N-LINKED (GLCNAC, ...) (POTENTIAL).

N-LINKED (GLCNAC, ...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                  Interpro; IPR002516; GT_11.
Pfam; Pf0131; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Golgi stack; Signal-anchor.
                                                                                                                                                                                                                                                                                                                                                                          Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kelly R.J., Rouquier S., Giorgi D., Lennon G.G., Lowe J.B.;
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                            -LINKED (GLCNAC. . .) (POR 135AC33F1B7B9F68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                          73.5%; Score 1393; DB 1; 78.8%; Pred. No. 2.1e-110;
                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                343 AA
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                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LKVFKPEAAFLPEWVGIPADLSPLLK 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
MEDLINE-95181460; PubMed=7876235;
MEDLINE-95181460; PubMed=7876235;
                                                                                                                                                                                                                                                                                                                                                                                                       25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKIFKPEAAFLPKWIGIPADLSPLLK
                                                                                                                                                                                                                                                                                                                                             39320 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primates;
                                                                                                                                       EMBL; X99620; CAA67931.1; -
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Mammalia; Eutheria;
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Best Local Simi
Matches 257;
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Q10981;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL), SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN). LUMENAL, CATALYTIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: CREATES A SOLUBLE PRECURSOR OLIGOSACCHARIDE FUC-ALPHA ((1,2)GALBETA-) CALLED THE H ANTIGEN WHICH IS AN ESSENTIAL SUBSTRATE FOR THE FINAL STEP IN THE SOLUBLE A AND B ANTIGEN SYNTHESIS PATHWAY. H AND SE ENZYMES FUCOSYLATE THE SAME ACCEPTOR
"Sequence and expression of a candidate for the human Secretor blood group alpha(1,2)fucosyltransferase gene (FUT2). Homozygosity for an enzyme-inactivating nonsense mutation commonly correlates with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PATHWAY: GLYCOSYLATION TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND BORGELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.

ALTERNATIVE PRODUCTS: TWO FORMS ARE PRODUCED BY THE USE OF ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.

TISSUE SPECIFICITY: SMALL INTESTINE, COLON AND LONG.

MISCELLANROUS: THERE ARE TWO GRNES (FUTI AND FUTZ) WHICH ENCODE GLACATOSIDE 2-1-FUCOSYLTRANSFERASE. THEY ARE EXPRESSED IN A GLACTOSIDE.

TISSUE-SPECIFIC MANNER WITH EXPRESSION RESTRICTED TO CELLS OF MESODERMAL OR ENDODERMAL ORIGIN RESPECTIVELY.

SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                                                  Kudo T., Iwasaki H., Nishihara S., Shinya N., Ando T., Narimatsu I.,
                                                                                                                                                                                                                                                                                                                               "Molecular genetic analysis of the human Lewis histo-blood group
System. In Secretor gene inactivation by a novel single missense
mutation A385T in Japanese nonsecretor individuals.";
J. Biol. Chem. 271:9830-9837(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 du Toit E.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBSTRATES BUT EXHIBIT DIFFERENT KM VALUES.
CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP alpha-L-fucosyl-1, 2-beta-D-galactosyl-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GALACTOSIDE 2-L-FUCOSYLTRANSFERASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Extensive polymorphism of the FUT2 gene in an African (Xhosa) population of South Africa."; Hum. Genet. 103:204-210(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pram: PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal-anchor; Golgi stack; Alternative initiation;
Blood group antigen; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Koda Y., Soejima M., Wang B., Kimura H., "Structure and expression of the gene encoding secretor-type galactoside 2-alpha-L-fucosyltransferase (FUT2).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu Y., Koda Y., Soejima M., Pang H., Schlaphoff T.,
Kimura H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND VARIANT PHE-140.
MEDLINE-97363210; PubMed=9219535;
                                                                                                                                                                                                 SEQUENCE FROM N.A., AND VARIANT PHE-140.
MEDLINE=96199252; PubMed=8621666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANTS VAL-25; CYS-138 AND ASN-172.
                                                                                                  non-secretor phenotype.";
J. Biol. Chem. 270:4640-4649(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eur. J. Biochem. 246:750-755(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98431007; PubMed=9760207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U17894; AAC24453.1; -.
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MIM; 182100; -.
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Hum. Genet. 10
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                                                                                                                                                                                                                                                                                                    Narimatsu H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAX-2000 (Rel. 39, Created)
30-MAX-2000 (Rel. 39, Last sequence update)
15-JOW-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 2 (EC 2.4.1.69) (GDP-L-fucose:beta-
D-galactoside 2-alpha-L-fucosyltransferase 2) (Alpha(1,2)FT 2)
(Fucosyltransferase 2) (FOT-III).
                                                                                                                                                                                                                                                                                                                                                                                                 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                GEYATLFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEER 120
                                                                                                                                                                                                                                                                                                                                             YRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPSTFV 180
                                                                                                                                                                                                                                                     11; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                GVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINAS
                                                                                                                                                                                                                                                                                                                                                                                                                         197 GVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIFVVTSNGMAWCRENIDTS
                                                                                            -> F (IN JAPANESE SEJ ALLELE; NON-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 (GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
                           (POTENTIAL)
                                                                                                                                                                                     DB 1; Length 343;
                R -> C (IN XHOSA POPULATION).
/FTId=VAR_003423.
                                                                                                                                D -> N (IN XHOSA POPULATION).
/FTId=VAR_003425.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lin B., Hayashi Y., Saito M., Sakakihara Y., Yanagisawa M.
Iwamori M.;
                                                                                                                                                                                                               Indels
                                                                                                                                                          12066D9CF175E13A CRC64;
                                                                                                                                                                                  Score 1386.5; DB 1;
Pred. No. 7.3e-110;
                                                                                                                      /FTId=VAR_003424.
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N-LINKED
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                                                                                                                                                          343 AA; 39017 MW;
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Matches 258; Conserv
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188
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                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 IPWQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAF 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-11 MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                     PATHWAY: Glycosylation.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
FORM IN TRANS CISTERNAE OF GOLGI (BY SIMILARITY).
MISCELLANEOUS: THERE ARE TWO GENES (FUT1 AND SEC1) WHICH ENCODE
GALACTOSIDE 2-L-FUCOSYLTRANSFERASE
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0C1-1996 (Rel. 34, Created)
01-0C1-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 2 (EC 2.4.1.69) (Secretor blood group alpha-2-fucosyltransferase) (GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase 2) (Alpha(1,2)FT 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
LUMBRAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
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Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4093E853EB37303B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.6%; Score 1338; DB 1;
88.0%; Pred. No. 9.9e-106;
Live 16; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286 DTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADL 321
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                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                              EMBL; Y09682; CAA71008.1; -.
EMBL; SAF113532; AAD25351.1; -.
MGD; MGI.109374; Fut2.
InterPro; IPR002516; GI_11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41464 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 stack.
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195
289
315
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195
185
389
315
368 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal-anchor;
DOMAIN
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Q10983;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                         FUCOSYLATE THE SAME ACCEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WHICH
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                                                                                    Hitoshi S., Kusunoki S., Kanazawa I., Tsuji S.;
"Molecular cloning and expression of two types of rabbit beta-
"Molecular cloning and expression of two types of rabbit beta-
galactoside alpha 1,2 fucosyltransferase.";
J. Biol. Chem. 270:884-8850(1955).
-!-FUNCTION. CREATES A SOUBLE PRECURSOR OLIGOSACCHARIDE FUC-ALPEA
((1,2)GALBETA-) CALLED THE H ANTIGEN WHICH IS AN ESSENTIAL
SUBSTRATE FOR THE FINAL STEP IN THE SOLUBLE A AND B ANTIGEN
SYNTHESTS PATHWAY. H AND SE ENZYMES FUCOSYLATE THE SAME ACCEPTOR
SUBSTRATES HOT EXHIBIT DIFFERENT KW VALUES.
-!-CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP +
alpha-L-fucosyl-1,2-beta-D-galactosyl-R = GDP +
                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- PATHWAY: Glycosylation.
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CLSTERNAR OF GOLGI.
-!- TISSUE SPECIFICITY: SALIVARY AND LACTATING MAMMARY GLANDS.
-!- MISCELLANGOUS: THERE ARE THREE GENES (FUT1, FUT2 AND FUT3) WHICH MISCELLANGOUS: THERE ARE THREE GENES (FUT1, FUT2 AND FUT3) WHICH MISCELLANGOUS: THERE ARE THREE GENES (FUT1, FUT2 AND FUT3) WHICH MISCELLANGOUS: THERE ARE THREE GENES (FUT1, FUT2 AND FUT3) WHICH MISCELLANGOUS GALACTOSIDE 2-L-FUCOSYLTRANSFERASE IN RABBIT. THEY ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 IPWQNYHLNDWMEERYRHIPGHEVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMBUNIL CATALYTIC (POTENTIAL).

N-LINKED (GLCNAC. ) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

1E2B831F9DA6CCB4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.1%; Score 1291; DB 1; 83.9%; Pred. No. 8.9e-102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 8.96
20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXPRESSED IN A TISSUE-SPECIFIC MANNER
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Pfam; PF01531; Glyco_transf_11; 1.
                                                            MEDLINE-95238380; PubMed=7721792;
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197
291
317
354 AA;
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Matches 235; Conserv
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal-anchor;
DOMAIN
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FUT1 RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                        225
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                                                                                                                                                 309
                                                                                                                                                                                                                                      RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3
                               15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 1 (EC 2.4.1.69) (GDP-L-fucose:beta-
D-galactoside 2-alpha-L-fucosyltransferase 1) (Alpha(1,2)FT 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.
FISSUE SPECIFICITY: IN THE ADULT, HIGHLY EXPRESSED IN PANCREAS, TESSTE SPECIFICITY: IN THE ADULT, HIGHLY EXPRESSED IN PANCREAS, TESTS AND EPIDIOYMIS AND TO A LESSER EXTENT IN THYMUS, LUNG, STOMACH, SMALL INTESTINE, COLON, SPLEEN AND UTERGS. NOT EXPRESSED IN BRAIN, HEART, SKELETAL MUSCLE, KIDNEY, LIVER AND BONE MARROW.
MISCELLANGOUS: THERE ARE TWO GENES (FUTI AND FOTZ) WHICH ENCODE GALACTOSIDE 2-L-PUCOSILTRANSFERASE.
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
LUMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
21F1D24CFE204106 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 ARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 AQLNGRQAFIQPEMHAALAPVFRISLPVLDPEVDSLTPWQHLVLHDWMSEEYSHLEDPFL 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 RFIGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVNGSQPS-TFVGVHVRRGD 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=NIH Swiss;

DOMINO S.E., Hiraiwa N., Lowe J.B.;

Domino S.E., Hiraiwa N., Lowe J.B.;

Molecular cloning, chromosomal assignment and tissue-specific expression of a murine alpha(1,2)fucosyltransferase expressed in thymic and epididymal epithelial cells.";

Biochem. J. 327:105-115(1997).

-: CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP alpha-L-fucosyl-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>ب</u>
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Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5e-86;
   376 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.3%; Score 1105.5; 62.8%; Pred. No. 4.5e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 376 51
67 67 N-
302 302 N-
328 328 N-
376 AA; 42255 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U90553; AAC53492.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                             PATHWAY: Glycosylation. SUBCELLULAR LOCATION: TI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Golgi stack.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR002516; GT_11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
   STANDARD;
                                                                                                                             (Fucosyltransferase 1).
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                                                                                                                                                            musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                NCBI_TaxID=10090;
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FUT1_MOUSE
009160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Sin
ses 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0cT-1996 (Rel. 34, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 1 (EC 2.4.1.69) (GDP-L-fucose:beta-
D-galactoside 2-alpha-L-fucosyltransferase 1) (Alpha(1,2)FT 1)
YVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAG 248
                                           NGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEA 308
                                                                                                                                                                                           285 NGQEGTPGKDFALLTQCNHTIMTIGTFGFWAAYLAGGDTVYLANFTLPDSEFLKIFRPEA 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FORM IN TRANS CISTERNAE OF GOLGI (BY SIMILARITY).

-!- MISCELLANBOUS: THERE ARE TWO GENES (FUT1 AND FUT2) WHICH ENCODE GALACTOSIDE 2-L-FOCOSYLTRANSFERAES. THEY ARE EXPRESSED IN A TISSUE-SPECIEL MANNER WITH EXPRESSION RESTRICTED TO CELLS OF MESODERMAL OR ENDODERMAL ORIGIN RESPECTIVELY.
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Piau J.-P., Labarriere N., Dabouis G., Denis M.G.;
"Evidence for two distinct alpha(1,2)-fucosyltransferase genes
differentially expressed throughout the rat colon.";
Blochem. J. 300:623-626(1994).
-!- CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GD
alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Two distinct rat GDP-L-fucose:b-D-galactoside 2-alpha-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fucosyltransferase genes.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   376 AA
                                                                                                                                                                                                                                                                                                     AFLPEWVGIPADLSPLLKALTPACPRSHFHL 339
                                                                                                                                                                                                                                                                                                                                                                           345 AFLPEWVGINADLSPLQAQFDPWKPDSLFRL 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Soejima M., Wang B., Koda Y., Kimura H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 169-310 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Golgi stack.
1 12
3 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L26009; AAB41514.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Fucosyltransferase 1). FUT1 OR FIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal-anchor;
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 1 (EC 2.4.1.69) (GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase 1) (Alpha(1,2)FT 1)
                                                                                                                                                                                                                                                                                                                                       247
                                                                                                                                                                                                                                                                                                                         GNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPE 307
                                                                                                                                                                         70 ARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFV 129
                                                                                                                                                                                                104 AQINGRRAFIQPEMHTTLAPVFRISLPVLDPEVDSLTPWQHLVLHDWMSEEYSHLEDPFL 163
                                                                                                                                                                                                                           187
                                                                                                                                                                                                                                                   223
                                                                                                                                                 PVAMVCLPYPSNASSGSPSCPE-----QSLLSGTWTITPGGRFGNQMGQYATLLAL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISCELLANEOUS: THERE ARE TWO GENES (FUT1 AND FUT2) WHICH ENCODE GALACTOSIDE 2-L-FUCOSYLITRANSFERASE. THEY ARE EXPRESSED IN A TISSUE-SPECIFIC MANNER WITH EXPRESSION RESTRICTED TO CELLS OF MESODERMAL OR ENDODERMAL ORIGIN RESPECTIVELY.
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.
TISSUE SPECIFICITY: BRAIN.
                                                                                                                                                                                                                          130 RFIGYPCSWIFYHHLRPEILKEFTLHDHVREEAQAFLRGLRVN--GSQPSTFVGVHVRRG
                                                                                                                                                                                                                                       DYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFA
                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                          PLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFAL
  LUMENAL, CATALYTIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

C350C737C758B7F8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rabbit beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11
                                                                        Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hitoshi S., Kusunoki S., Kanazawa I., Tsuji S.,
"Molecular cloning and expression of two types of rabbit be
galactoside alpha 1.2-fucosyltransferase.";
J. Biol. Chem. 270:8844-8850(1995).
-!- CATALYTIC G. G.DP-L. fucose + beta-D-galactosyl-R
alpha-L.fucosyl-1,2-beta-D-galactosyl-R.
-!- PATHWNY: Glycosylation.
 CATALYTIC (POTENTIAL)
                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
                                                                          DB 1;
                                                                        58.1%; Score 1101.5; DB 1
62.3%; Pred. No. 9.8e-86;
tive 37; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                373 AA
                                                                                                                                                                                                                                                                                                                                                                             AAFLPEWVGIPADLSPLLKALTPACPRSHFHL 339
                                                                                                                                                                                                                                                                                                                                                                                                  344 AAFLPEWVGINADLSPLQAQFDPWETDSLFRL 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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MEDLINE=95238380; PubMed=7721792;
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                                                     42416
                                                                                                     207; Conservative
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     376
64
302
328
     30
64
302
328
376 AA;
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                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUT1_RABIT
     DOMAIN
CARBOHYD
CARBOHYD
                                        CARBOHYD
                                                                            Query Match
                                                     SEQUENCE
                                                                                           Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               010979;
                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
FUT1_RABIT
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JNN-2002 (Rel. 41, Last annotation update)
6alactoside 2-fucosyltransferase 1 (EC 2.4.1.69) (GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase 1)
6Fucosyltransferase 1) (Blood group H alpha 2-fucosyltransferase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 YVHVMPNVWKGVVADDRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAG 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 LPVTSPASNASSCAGRPAAPS------GIWTIHPDGRFGNOMGOYATLLALA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 NGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 LPMTTQMS-----SGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LUMBNAL, CÁTALYTIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                   Interpro: IPR002516; GT_11.
Pfam: PF01031; G1yCo_transf_11; 1.
Transferase: G1yCoyltransferase; G1ycoprotein; Transmembrane: Signal-anchor; G01g1 stack.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.0%; Score 1080.5; DB 1; Length 373; 63.3%; Pred. No. 5.8e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0A47A1786231525C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51;
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SEQUENCE FROM N.A., AND VARIANT ALLELES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
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66 66
301 301
327 327
373 AA; 42098 M
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                                                                                                                                                                                                                               EMBL; X80226; CAA56513.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 200; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  733
                                                                                                                                                                                                                                                                                                                                                                                                           Signal-anchor;
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUT1_HUMAN
P19526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                               Koda Y., Soejima M., Johnson P.H., Smart E., Kimura H.;

Missense mutation of FUT1 and deletion of FUT2 are responsible for

Indian Bonday Phenotype at ABO blood group system.";

Biochem. Biophys. Res. Commun. 238:21-25(1997).

-!- FUNCTION: CREATES A SOLUBLE PRECURSOR OLIGOSACCHARIDE FUC-ALPHA

((1,2)GALBETA-) CALLED THE H AWTIGEN WHICH IS AN ESSENTIAL

SUBSTRATE FOR THE FINAL STEP IN THE SOLUBLE A AND B ANTIGEN

SUBSTRATES BUT EXHIBIT DIFFERENT KM VALUES.

-!- CATANTY CATIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP +

alpha-L-fucosyl-1,2-beta-D-galactosyl-R.

-!- SUBSELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
LUMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FORM IN TRANS CISTERNAE OF GOLGI.
POLYMORPHISM: NONFUNCTIONAL MUTANT OF FUT1 ARE THE CAUSE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MISCELLANEOUS: THERE ARE TWO GENES (FUT1 AND FUT2) WHICH ENCODE GALACTOSIDE 2-L-FUCOSYLTRANSFERASE. THEY ARE EXPRESSED IN A TISSUE-SPECIFIC MANNER WITH EXPRESSION RESTRICTED TO CELLS OF
                                                                                                                                                                             Molecular basis for H blood group deficiency in Bombay (Oh) and
                                                                                                                        MEDLINE-94286534; PubMed-7912436;
Kelly R.J., Ernst L.K., Larsen R.D., Bryant J.G., Robinson J.S.
Lowe J.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harm, 201531; Glyco_transf_11; 1.

Pfam: PF01531; Glyco_transf_11; 1.

Pfam: PF01531; Glyco_transf_11; 1.

Signal anchor; Golgi grack; Polymorphism; Blood group antigen.

DOMAIN 1 CYTOPLASMIC (POTENTIAL).

TRANSMEM 9 25 SIGNAL-ANGHOR (TYPE-II MEMBRANE PI DOMAIN 26 365 LUMBRAL, CATALYPIC (POTENTIAL).

CARBOHYD 65 65 N-LINKED (GLCNAC. ..) (POTENTIAL).

CARBOHYD 327 327 N-LINKED (GLCNAC. ..) (POTENTIAL).
                                 "Polymorphism of the h allele and the population frequency of sporadic nonfunctional alleles."; Iransfusion 37:284-290(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /FTId=VAR_003417.
L -> H (IN PARA-BOMBAY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. ) Y \rightarrow C (IN BOMBAY H-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /FTId=vAR_009708.
W -> C (IN BOMBAY H-).
/FTId=vAR_003418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> R (IN BOMBAY H-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> E (IN BOMBAY H-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -> V (IN BOMBAY H-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W -> C (IN BOMBAY H-).
                                                                                                                                                                                                para-Bombay individuals.";
Proc. Natl. Acad. Sci. U.S.A. 91:5843-5847(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MESODERMAL OR ENDODERMAL ORIGIN RESPECTIVELY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VAR_009709
                                                                                                                                                                                                                                                                    MEDLINE=97445117; PubMed=9299444;
MEDLINE=97240210; PubMed=9122901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M35531; AAA52639.1; -.
EMBL; Z69587; CAA93435.1; -.
                    Wagner F.F., Flegel W.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BOMBAY BLOOD GROUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGNC:4012; FUT1.
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01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
6alactoside 2-L-fucosyltransferase 1 (EC 2.4.1.69) (GDP-L-fucose:beta-D-galactoside_Z-alpha-L-fucosyltransferase 1) (Alpha(1,2)FT 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 GTAMGPNASSSCPQH-PASLSGTWTVYPNGREGNQMGQXATLLALAQLNGRRAFILPAMH 117
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                                                                                                                                                                                                                                                                                                                             GNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMH 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Meijerink E., Neuenschwander S., Fries R., Dinter A., Meijerink E., Neuenschwander S., Voegeli P.; Merschinger H.U., Stranzlinger G., Voegeli P.; Merschinger H.U., Stranzlinger G., Voegeli P.; Merschinger H.U., Stranzlinger G., Voegeli P.; Merschinger H.U., Stranzlinger G. Voegeli P.; Merschinger H.G., Stranzlinger G. Voegeli P.; Merschinger G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI_TaxID=9823;
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M
                                                                                                                                             DB 1; Length 365;
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/FIId=VAR_003421.
4F4442EC375C9D9E CRC64;
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Cohney S., Mouhtouris E., McKenzie I.F., Sandrin M.
"Molecular cloning of the gene coding for pig alpha
                                                                                                                                   55.5%; Score 1051.5; DB 1; 63.3%; Pred. No. 1.6e-81; live 37; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                365 A.A.
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                                                41251 MW;
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                                                                                                                                   Query Match 55.5%
Best Local Similarity 63.3%
Matches 195; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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01-NOV-1997 (Re.
                                                SEQUENCE
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SEQUENCE FROM N.A.
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P34302;
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CARBOHYD
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                                                                                                                between the Swiss Institute of Bioinformatics and the EMBL outstation—
the European Bioinformatics Institute. There are no restrictions on its
work by non-profit institutions as long as its content is in no way
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or send an email to license@isb-sib.ch).
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                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                        SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
LUMERAL, CATALYIIC (POTENTIAL).
LUNELINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 AFIPASMHNALAPIFRISLPVLHSDTAKKIPWQNYHLNDWMEERYRHIPGHFVRFTGYPC 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 PMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRL 76
            PATHWAY: Glycosylation.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
FORM IN TRANS CISTERNAE OF GOLGI.
MISCELLANBOUS: THERE ARE TWO GENES (FUTL AND FUT2) WHICH ENCODE
GALACTOSIDE 2-L-FUCOSYLTRANSFERASE. THEY ARE EXPRESSED IN A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 2 (EC 2.4.1.59) (Secretor blood group alpha-2-fucosyltransferase) (GDP-L-fucose:beta-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWTFYHHLRPEILKEFILHDHVREEAQAFLRGLRV--NGSQPSTFVGVHVRRGDYVHVMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 SWIFFHHLREQIRSEFILHDHLRQEAGGVLSQFRLPRIGDRPSTFVGVHVRRGDYLRVMP
                                                                                                                                                                                                         EMBL; U70883; AAB81884.1; -.
EMBL; AF136896; AAF58933.1; -.
Interpreto; IPR002516; GI_11.
Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                          55.4%; Score 1050.5; DB 1; Length 365; 62.9%; Pred. No. 1.9e-81;
                                                                    TISSUE-SPECIFIC MANNER.
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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R -> Q.
L -> F (IN REF. 1).
DAFCE77E89A29D75 CRC64;
                                                                                                                                                                                                                                                                  Ĝolgi stack; Polymorpĥism.
1 8 CYTOPLASMIC (POTENTIAL).
alpha-L-fucosyl-1,2-beta-D-galactosyl-R
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 38;
                                                                                                                                                                                                                                                                                                                                                                                    41106 MW;
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365
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                                                                                                                                                                                                                                                                    Signal-anchor;
DOMAIN
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Q10984;
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VARIANT
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Biochem. J. 300:623-626(1994).

-!- FUNCTION: CREATES A MEMBAAN.
--- SSOCIATED PRECURSOR OLIGOSACCHARIDE
FUC-ALPHA((1,2)GALBETA-) CALLED THE H ANTIGEN WHICH IS AN
ESSENTIAL SUBSTRATE FOR THE FINAL STEP IN THE MEMBRANE. ASSOCIATED
A AND B ANTIGEN SYMPHESIS PATHWAY. H AND SE ENZYME FUCOSYLATE
THE SAME ACCEPTOR SUBSTRATES BUT EXHIBIT DIFFERENT KM VALUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEW 120
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                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rođentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP + alpha-L-fucosyl-1.2-beta-D-galactosyl-R.

-i alpha-L-fucosyl-1.2-beta-D-galactosyl-R.

-i PATHWAX: Glycosylation:
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROFIEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLG! (BY SIMILARITY).

-!- MISCELLANEOUS: THERE ARE TWO GENES (FUT1 AND FUT2) WHICH ENCODE GALACTOSIDE 2-L-FUCOSYLTRANSFERASE. THEY ARE EXPRESSED IN A
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14DECEB7C2E6384A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        Plau J.-P., Labarriere N., Dabouis G., Denis M.G.;
"Evidence for two distinct alpha(1,2)-fucosyltransferase genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transferase; Glycosyltransferase; Glycoprotein; Transmembrane
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SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11
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pred. No. 1.4e-64;
); Mismatches 1; Indels
galactoside 2-alpha-L-fucosyltransferase 2) (Alpha(1,2)FT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  315 VGIPADLSPLLKALTPACPRSHFHLKAKGVTCYVAGRAF 353
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0; Mismatches
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Pfam; PF01531; Glyco_transf_11; 1.
                       (Fucosyltransferase 2) (Fragment) FUT2 OR SEC1 OR FTB.
                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94280382; PubMed=8010942;
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159 AA; 17250 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.68;
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Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L26010; AAB41515.1;
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                                                                                                         Rattus norvegicus (Rat).
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VGLD_HSVEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                         Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Faveln A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 STARLANHIFELVSVYGMAKSLNRKPAIFVEDSKYNLLITGVRKVLPGLLDEFQIFEYPV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 --TAKKIP------WQNYHLNDWMEERYRHIPGHFVRFTGYPCSWTFYHHLRPEILKEF 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                j.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153 TLHDHVREEAQAFLRGL----RVNGSQPSTFVG---VHVRRGDYV---HVMPNVWKGVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---YSSPVFVVTSNGMAWCRENINASRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 VVFAGNGIEGSPAKDFALL-TQCNHTIMTI--GTFGIWAAYLAGGDTIYLANY-TLPDSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               224 --SFIKPALEFIKEREOKDVNKKMLTVIMGDDPDFEAKMF----EGTVRAKKEAKIEETT
                                                                                                                                                                                                                                                                οĘ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 HNKATKVPLSEKCCIFDNPDKFNNISSEYLHLTGHFYQ-----SWKYF-----
                                                                                                                                                                                                                                                               2.2 Mb of contiguous nucleotide sequence from chromosome III
                                                                                                                                                                                                                                                                                                                                              Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 168; DB 1; Length 365;
Pred. No. 7.3e-07;
8; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 SIGRLGNOMGEYATLFALARMNGR--LAFIPASMHNALAPIFRISLPVLHSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01531; Glyco_transf_11; 1.
Hypothetical protein; Transferase; Glycosyltransferase.
SEQUENCE 365 AA; 41991 MW; B5FBCA363F31977F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Pred. No. 7.3e-
48; Mismatches
                                                                                STRAIN=Bristol N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 FLK-VFKPEAAFLPEWVGIPAD 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WormPep; C06E1.7; CE30483.
InterPro; IPR002516; GT_11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 22.09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L16559; AAA27932.2;
                                                                                                                                                                                                                                                                                          Nature 368:32-38(1994).
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203 DRGYLEKALDMFRAR-
                                        NCBI_TaxID=6239;
                                                                                                                                                                                                                                                  Wohldman P.;
                                                                                                                                                                                                                                                                                                                                    Waterston R.
                                                                                                                                                                                                                                                                                                                    REVISIONS
                                                                                                                                                                                                                                                                             elegans
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RESULT 13

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                    Flowers C.C., Eastman E.M., O'Callaghan D.J., "Sequence analysis of a glycoprotein D gene homolog within the unique short segment of the EBY-1 genome."; Virology 180:175-184(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 NSIGRLGNOMGEYAT--LFALARMNGRLAFIPASMHNALAPIFRISLPVLHSDTAKKIPW 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 QNYHLNDWMEERYRH----IPGHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQ 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    288 RFLGEFNFPQGEHMTWVKFWFVYDGGNL---PVQFYEAQA---------FARPVƏP 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    332 DNHPGFDSVESEITQNKTDPKPGQADPKPNQPFKWPSIKHLVPRL-----DEVDEVIE 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LQQRIVKLQ------PLSEKELPMTTQMSSGNTESPEMRRDSEQHGNGELRGMFTI 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE=92263758; PubMed=1316673;
Colle C.F. III, Flowers C.C., O'Callaghan D.J.,
"Open reading frames encoding a protein kinase, homolog of allycoprotein gx of pseudorabies virus, and a novel glycoprotein map within the unique short segment of equine herpesvirus type 1."; Virology 188:545-557(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         164 AFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSP 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.8%; Score 91; DB 1; Length 442; 22.7%; Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                   Equine herpesvirus type 1 (strain Kentucky A) (EHV-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323CDCA9C9762F05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                      Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Varicellovirus.
                                              01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Glycoprotein D precursor (Glycoprotein 17/18).
GD OR GP17/18 OR 72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL. GLYCOPROTEIN D.
442 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002896; Herpes_glycop_D. Pfam; PF01537; Herpes_glycop_D; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M86931; -; NOT_ANNOTATED_CDS.
EMBL; M87497; AAA46073.1; ALT_INIT.
PRT;
                                                                                                                                                                                                                                                                                                                                              PubMed=1845821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49908 MW;
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STANDARD;
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422
422
103
111
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A38518; VGBEEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111
347
396
442 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=91082407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54;
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DOMAIN
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STANDARD;
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PDB; 1D7D; 18-OCT-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                       CDH_PHACH
Q01738; 000047;
                                                                                                                                                                                                                                                                                                                                     CDH-1 AND CDH-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=OGC101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Divne C.;
                                                                                                                                                                  RESULT 15
CDH_PHACH
                                  g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bidinformatics and the BEBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIPNGAYSPANYTHVDWLGRDYTEIGAATVNTPKGF----YVLESTYAQNAGLRPTILC 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 LTTELTEGNQEAAGLIMTAEPVEVTLVAGN-----NYYGYDGSQGGNQISQGTPLE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                      Fujiwara T., Morishima S., Takahashi I., Hamada S., "Molecular cloning and sequencing of the fimbrilin gene of Porphyromenas gingivalis strains and characterization of recombinant proteins."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Finbrillin is the structural subunit of the fimbriae, that are filamentous appendages on the cell surface. Fimbriae of P. gingivalis are recognized as a major virulence factor as they mediate cell adhesion and play an important role in invasion of
385 PVTKPPKTSKSN-STFVGISVGLGIAGLVLVGVILYVCLRR---KKELKVCTERLDSP 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
MAJOR FIMBRIAL SUBUNIT PROTEIN, TYPE
, 7FBE4FBF427FBA2AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 MTTQMSSGNTESPEMRRDSEQ-----HGNGELRGMFTINSIGRLGNQMG---EYATLFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----IPWQNYHINDWMEERYRHI-----PGHFVRFTGYPCSWTFYHH--LRPEIL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 LARMNGRLAF--IPASMHNALAPIFRISLPVLHSDTAKK------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Functional differences among Finh variants of Porphyromonas gingivalis and their effects on adhesion to and invasion of human \ensuremath{\mathsf{Municonst}}
                                                                                                                                             15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Major fimbrial subunit protein, type III precursor (Fimbrillin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             periodontal tissues.
SUBCELLULAR LOCATION: Fimbria.
SIMILARITY: BELONGS TO THE P.GINGIVALIS FIMBRILLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nakagawa I., Amano A., Kuboniwa M., Nakamura T., Kawabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38; Mismatches 110; Indels
                                                                                                                                                                                                                                        gingivalis).
Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem. Biophys. Res. Commun. 197:241-247(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION, AND CLASSIFICATION INTO TYPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.7%; Score 89; 22.1%; Pred. No.
                                                                                                                                                                                                                                      Porphyromonas gingivalis (Bacteroides Bacteria; Bacteroides;
                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21614934; PubMed=11748193;
                                                                                                                                                                                                                                                                               Porphyromonadaceae; Porphyromonas.
                                                                                                                                                                                                                                                                                                                                                     STRAIN=6/26;
MEDLINE=94071950; PubMed=7902712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 epithelial cells.";
Infect. Immun. 70:277-285(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         353 Mi
38024 MW;
                                                                                                                            15-JUN-2002 (Rel. 41, Created)
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                                                                                           STANDARD;
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353 AA;
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                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                NCBI_TaxID=837;
                                                                                                                                                                                                     (Fimbrilin).
                                                                                       FMA3_PORGI
Q51826;
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Best Local 3
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics. Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li B., Negalia S.R., Renganathan V.:
"Ce.ibblose dehydrogenase from Phanerochaete chrysosporium is encoded
by two allelic variants.";
Appl. Environ. Microbiol. 63:796-799(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hallberg B.M., Bergfors T., Boeckbro K., Pettersson G., Henriksson G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: DEGRADES BOTH LIGNIN AND CELLULOSE. OXIDIZES CELLOBIOSE TO CELLOBIONOLACTONE.
--KEFTLHDHV----REEAQAFLRGLRVNGSQPSTF--VGVHVRRGDYVHVMPNVWKGVV 201
                                  246 VKGKLTKHDGTALSSEEMTAAFNAGWIVANNDPTTYYPVLVNFESNNYTYTGEAVEKGKI 305
                                                                                                                                                                                                                                                                                                                                                       Phanerochaete chrysosporium.
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Aphyllophorales; Corticiaceae; Phanerochaete.
NCBI_TaxID=5306;
                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
31-MAY-2002 (Rel. 41, Last annotation update)
Cellobiose dehydrogenase precursor (EC 1.1.5.1) (CDH) (Cellobiose-quinone oxidoreductase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A new scaffold for binding haem in the cytochrome domain of extracellular flavocytochrome cellobiose dehydrogenase."; Structure 8:79-88(2000).
                                                                                                 306 VRNHKFDINLTITGPGTNNPENPIT-----ESANLNVCVAAMKGV 347
                                                                          202 ADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGI 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Li B., Nagalla S.R., Renganathan V.; "Cloning of a cDNA encoding cellobiose dehydrogenase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hemoflavoenzyme from Phanerochaete chrysosporium.";
Appl. Environ. Microbiol. 62:1329-1335(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 19-208 MEDLINE=20139694; PubMed=10673428;
                                                                                                                                                                                                              773 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lactone + a phenol.
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MEDLINE=97176414; PubMed=9023960;
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InterPro; IPR001100; Pyr_redox.
Pfam; PF00732; GMC_oxred; 1.
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11;
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                                                                                                                                                                                                                               337 GDFSSSVGWPSSWINHAPYTSKLSSRLPSTDHPSTDGQRYLEQSFNVVSQLLKGQGYNQA 396
                                                                                                                                                                                                                                                                                                      238 ----NASRGDVVFAGNGIEGSPAKD-----FALLTQCNHTIMTIGTFG----IWAAYL 282
                                                                                                                                                                                                            126 GHFVRFTGYPCSWTFYHHLRPEILKEFTLHDHVREEAQAFLRG------LRVNGSQPS 177
                                                                                                                                                                                                                                                        178 TFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENI 237
                                                                                                                                                                                                                                                                           397 T------INDNPNYKDHVF---GY--SAFDFLNGKRAGPVATYLQTALA--RPNF 438
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Search completed: May 27, 2003, 15:07:14 Job time: 11.3317 secs

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Pig secretor. Sus
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Rat hepatoma H35 c
Rat hepatoma H35 c
Swine alpha(1,2) f
Swine alpha 1,2-fu
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Human Sec2 protein
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1 MLVVQMPFSFPMAHFILEVF......AAFLDFEWTGIAADLSPLLKH 344
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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######################################	5 12 AAR13751 GDP-Fuc:beta-D- 5 16 AAR0154 GDP-L-fucose-be 5 16 AAR70422 2-Alpha-fucosyl 5 16 AAR70421 2-Alpha-fucosyl 5 17 AAR90572 Human H-transfe 5 18 AAW23805 Human alpha 1,2	5 18 AAN13040 Human alpha(1,2)- 5 1 AAV97279 Human H-transferase 5 19 AAV93102 Pig H-transferase 5 21 AAV9302 Pig alpha-1-2 fuc 5 23 AAB47995 Swine alpha (1,2) 5 15 AAR45936 A glycosyltransfe 7 20 AAX17969 X. laevis alpha-1-0 21 AAO03530 Human secreted or	7 23 AAM51992 Bacteroides fraging 0 21 AAY92713 H. pylori uA802 at pylori uA802 at pylori 2 AAK92124 Helicobacter pylori 5 18 AAW22124 pig alpha 1-6 fuc 5 23 ABG34136 Antibody producti 1 22 AAG39722 Propionibacterium 5 22 AAG73884 Human colon cance 3 12 AAR15057 Cytochrome p450c2	5 18 AAW22125	8 21 AAY51120
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New rat ganglioside GMI-specific alphal-2Fucosyltransferase, useful for preparation of fucosyl GMI which is useful as a nutritional composition
                                                                                                                    Human; Sec2; alphal-2fucosyltransferase; cytostatic;
neuroprotective; nootropic; gene therapy; Fucalphal-2Galbetal-3GalNAc;
immunotherapy; immunosuppression; cancer; neurological disease;
                                                                                                                                                                                                                                                                                                        (PACI-) PACIFIC NORTHWEST CANCER FOUND
                      AAB36106 standard; Protein; 344 AA.
                                                                                            Human Sec2 catalytic domain.
                                                                                                                                                                                                                                                                                99WO-US07384
                                                                                                                                                                                                                                                         99WO-0S07384
                                                                     (first entry)
                                                                                                                                           immunotherapy; immunosupp
small cell lung carcinoma
                                                                                                                                                                                                                                                                                                                              Holmes EH, Sherwood AL;
                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-687262/67.
                                                                                                                                                                                                       WO200064464-A1.
                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                        23-APR-1999;
                                                                   19-FEB-2001
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                                              AAB36106;
RESULT 1
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28-AUG-1998
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                   (KELL/)
(LENN/)
(LOWE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
δŏ
                                         The present sequence is given in a specification relating to a rat ganglioside GM 1-specific alphal-2fucosyltransferase protein. The protein or its cellular fraction is useful for synthesis of a molecule comprising curalphal-2calbetal-3GalNac.

The method involves contacting alphal-2fucosyltransferase with GDP-fucose or a free oligosaccharide comprising Fucalphal-2Galbetal-3GalNac.

The method involves contacting alphal-2fucosyltransferase with GDP-fucose or a precipited sylvoprotein, glycolipoprotein or oligosaccharide having a terminal Galbetal-3GalNac group. It is also useful for synthesis of fucosyl-GM_1 by contacting the protein with GDP-fucose and ganglioside GM_1. The obtained glycoproteins.

Inunuotherapeutic or immunosuppressive action against cancer, neurological disease or small cell lung carcinoma.
                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                   240
                                                                                                                                                                                                                                                                                                                                                                                                                                                             VVTSNGMAWCRENIDISHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAXLT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHDHVREEAQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                             61 RGMWIINAIGRLGNQMGEXATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATAS
                                                                                                                                                                                                                                                                                 1 MLVVQMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAMWELPVQIPVLASTSKALGPSQL
                                                                                                                                                                                                                                                                                                 Score 1850; DB 21; Length 344; pred. No. 2.5e-186;
   or immunotherapeutic for cancer and neurological diseases
                                                                                                                                                                                                                                                            Indels
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                         Example; Fig 3B; 91pp; English.
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al Similarity 100.0%;
344; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Sec2 protein sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                     344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US5807732-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW69332;
                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                          Query Match
Best Local 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301
                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW69332
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This sequence is the human Sec2 protein of the invention. The DNA encodes a alpha(1,2) fucosyltransferase and is the Secretor alpha(1,2)fucosyltransferase and is the Secretor the DNA is useful for Hood group alpha(1,2)fucosyltransferase gene. The DNA is useful for producing a recombinant human GDP-L-fucose.beta-D-galactoside 2-alpha-L-fucosyltransferase (FUT2) which can be used for genotyping an individual as a secretor or nonsecretor as it is known that nonsecretors homozygous for a mutant allele of the FUT2 gene that has a stop codon in the position corresponding to amino acid 143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 VVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWANLT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHDHVREEAQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATAS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                               recombinant enzyme and genotyping person as secretor or nonsecretor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MLVVQMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAMWELPVQIPVLASTSKALGPSQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 19; Length 343;
                                                                                                                                                                                                                               producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Secretor; glycosyltransferase; FUI2; pig; epitope; antigen;
transgenic animal; xenotransplantation; organ transplant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 344
                                                                                                                                                                                                                               DNA encoding fucosyltransferase enzyme - useful for
                                                                                                                             Rouguier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1832.5; DB 1
Pred. No. 1.8e-184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                             Lennon G, Lowe JB,
                                                                                                                                                                                                                                                                                                   Disclosure; Column 45-50; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Porcine secretor transferase (FUT2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW37855 standard; Protein; 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 99./
Matches 343; Conservative
                                                                                                                               Giorgi D, Kelly RJ,
                                                                                                                                                                      WPI; 1998-520127/44.
N-PSDB; AAV58323.
GIORGI D.
KELLY R J.
LENNON G.
LOWE J B.
ROUQUIER S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       343 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This polypeptide comprises porcine secretor glycosyltransferase (SE or FUT2), a type II integral membrane protein has high affinity for type I and type III substrates. Its amino acid sequence was deduced from the nucleotide sequence of a genomic DNA clone (see AAV29003) isolated from a pig liver library on the basis of homology to human FUT2 cDNA. Pig FUT2 shows 81.2% identity with human FUT2. Expression of a glycosyltransferase, such as porcine Se, in a tissue results in reduced expression of unwanted carbohydrate epitopes on the tissue, especially porcine heart, liver, kidney or pancreas, rendering it more suitable for transplantation, i.e. less immunogenic and of increased immunological acceptability. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MLVVQMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAMWELPVQIPVLASTSKALGPSQL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    claimed method of producing a cell from a donor species that is immunologically acceptable to a recipient species involves reducing levels of carbohydrate on the donor cell that causes it to be recognised as non-self by the recipient by expressing a nucleic acid for a glycosyltransferase such as porcine Se in the cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHDHVREEAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid encoding glycosyltransferase able to compete with second such enzyme - particularly used to reduce expression of unwanted carbohydrate epitope(s) on tissues intended for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                              /note= "N-terminal cytoplasmic tail"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.6%; Score 1528; DB 19;
82.0%; Pred. No. 2.3e-152;
ive 24; Mismatches 34;
                                                                                                                                                             279..281
/note= "Asn is N-glycosylated"
                                                                                                                       /note= "Asn is N-glycosylated"
                                                                                                                               /noce
251..253
/note: "Asn is N-glycosylated"
                                                                                                                                                                                                               /note= "Asn is N-glycosylated"
                                                            'note= "transmembrane domain"
                                                                  /note= "C-terminal domain"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Fig 1A-B; 40pp; English.
                                                                                                                                                                                                                                                                                                          97WO-AU00540
                                                                                                                                                                                                                                                                                                                                      96AU-0001823
                                                                                                                                                                                                                                                                                                                                                                                                   McKenzie IFC, Sandrin MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          282; Conservative
                                                                                                                                                                                                                                                                                                                                                                   (AUST-) AUSTIN RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-169148/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               340 AA;
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                                                                                                       Modified-site
                                                                                                                                    Modified-site
                                                                                                                                                                    Modified-site
                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                            WO9807837-A1
                                                                                                                                                                                                                                                                                                        22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                      23-AUG-1996;
                                                                                                                                                                                                                                                                           26-FEB-1998
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                                              Domain
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                 Domain
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             KFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIF 240
                                                       VVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                       Nucleic acids encoding chimeric glycosyltransferases - used for altering carbohydrate levels on the surface of cells, useful in therapy and transplantation
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7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 340;
                                                                                                                                                                                                                                                                                                                                secretor; chimeric; glycosyltransferase; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                              301 GGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.6%; Score 1528; DB 19;
82.0%; Pred. No. 2.3e-152;
iive 24; Mismatches 34;
                                                                                                                                                                                                               AAW53101 standard; Protein; 340 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Fig 6; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transplantation or gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            97WO-AUG0492.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96US-0024279.
                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sandrin MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 82.09
Matches 282; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AUST-) AUSTIN RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-159170/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            340 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAV21639
                                                                                                                                                                                                                                                                                                                                              transplantation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McKenzie IFC,
                                                                                                                                                                                                                                                                                                                                                                                                     W09805768-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1997;
                                                                                                                                                                                                                                                                                                    Pig secretor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-AUG-1996;
                                                                                                                                                                                                                                                                      08-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                 12-FEB-1998.
                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa.
                                                                                                                                                                                                                                           AAW53101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
181
                         177
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AAW53101
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Holmes EH,
                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence was given in a specification relating to an isolated rat ganglioside GM_-specific alphal-2fucosyltransferase protein. The protein or its cellular fraction is useful for synthesis of a molecule comprising Fucalphal-2Galbetal-3GalRAC, a glycolipid, glycoprotein, glycolipoprotein or a free oligosaccharide comprising Rucalphal-2Galbacal-3GalRAC. The method involves contacting alphal-2fucosyltransferase with GDP-fucose and a molecule or glycolipid, glycoprotein, glycolipoprotein or oligosaccharide having a terminal dabetal-3GalRAC group. It is also useful for synthesis of fucosyl GM_I by contacting the protein with GDP-fucose and ganglioside GM_I The obtained glycoproteins, glycolipoproteins, glycolipids and fucosyl-GM_I configurate are useful as nutritional compositions and fucosyl-GM_I configurate are useful as nutritional compositions and fucosyl-GM_I configurate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New rat ganglioside GMI-specific alphal-2Fucosyltransferase, useful for preparation of fucosyl GMI which is useful as a nutritional composition or immunotherapeutic for cancer and neurological diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is useful for inducing an immunotherapeutic or immunosuppressive action against cancer, neurological disease or small cell lung carcinoma.
RGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATAS 120
                         117
                                                  180
                                                                         176
                                                                                                 240
                                                                                                                                                 300
                                                                                                                                                                     237 VVSSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTVMTIGTFGIWAAYLA 295
                                                                                                                                                                                                                                                                                                                                                                                Rat; alphal-2fucosyltransferase; cytostatic; neuroprotective; nootropk; gene therapy; Fucalphal-2Galbetal-3GalNAc; immunotherapy; fimmunosuppression; cancer; neurological disease; small cell lung carcinoma.
            VVTSNGMAWCRENIDISHGDVVFAGDGIEGSPAKDFALLTQCNHIIMIGTFGIWAAYLT
                                                                                                KFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIF
                                               RIPWQNYHLNDWMEEEYRHIPPGEYVRFTGXPCSWTFYHHLRQEILQEFTLHDHVRBEAQ
                                                                                                                                                                                              GGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 344
                                                                                                                                                                                                           H35 cell alphal-2fucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PACI-) PACIFIC NORTHWEST CANCER FOUND.
                                                                                                                                                                                                                                                                                  AAB36104 standard; Protein; 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 5; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US07384.
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                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Holmes EH, Sherwood AL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-687262/67.
N-PSDB; AAC67965.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200064464-A1.
                                                                                                                                                                                                                                                                                                                                                        Rat hepatoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-APR-1999;
                                                                                                                                                                                                                                                                                                                                  19-FEB-2001
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                                                                                                                                                                                                                                                                                                         AAB36104;
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 61
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AAB36104
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                                                                                                                                                                                                                             Rat; alphal-2fucosyltransferase; alphal-2fucT; antisense therapy; galactose betal-3N-acetylgalactosamine; Galbetal-3GalNac; glycolipid; glycoprotein; glycolipoprotein; oligosaccharide; fucosyl-GM1; cancer; gene therapy; oncogenic transformation; cytostatic; ganglioside; GM1; cell transformation
                                                                                                                                                                 9
                                                                                   Gaps
                                                                                                                        MLVVQMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAM--WELPV-----QIPVLA 49
                                                                                                                                                                                                                                                                                                            SIPVLHSDTARKIPWQNYHLNDWMEERYRHI-PGHFVRFTGYPCSWTFYHHLRPBILKRE
                                                                                                                                                                                                                                                                                                                                                                                              1 MASAQVPFSFPLAHFLIFVFVTSTIIHLQQRIVKLQPLSEKELPMTTQMSSGNTESPEMR
                                                                                                                                                                                                       STSKALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRI
                                                                                                                                                                                                                                                                                       110 TLPVLHSATASRIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEF
                                                                                                                                                                                                                                                                                                                                                                      TLHDHVREEAQKFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALD
                                                                                                                                                                                                                                                                                                                                                                                                                                                      230 WFRARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 MFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLIQCNHTIMII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                353
                                                                                 12;
                                          380;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Intracellular/Transmembrane domain"
                                          Length
                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Region which overlaps rat
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                                        Score 1475; DB 21;
Pred. No. 1.1e-146;
                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat hepatoma H35 cell alphal-2FucT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE16622 standard; Protein; 380 AA
                                                                               30;
                                      79.78;
77.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ...380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sherwood AL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               661
                                                            Similarity
380 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE16622;
Sequence
                                        Query Match
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99WO-0S07384

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Rat; alphal-2fucosyltransferase; cytostatic; neuroprotective; nootropic; gene therapy; Fucalphal-2Galbetal-3GalNAC; immunotherapy; immunosuppression; cancer; neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                            Rat hepatoma H35 cell alphal-2fucosyltransferase catalytic domain.
                                                                                                                                                                                                                                                                                                                                                                                      AAB36105 standard; Protein; 353 AA
                                                                                                                                                                                                                                                                                                                                                                                                               19-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              small cell lung carcinoma.
                        Rat hepatoma H35
GM1-specific alph
                                                                                                                                                       alphal-2FucT.
                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                   AAB36105;
                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                      300
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Rattus norvegicus

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(PACI-) PACIFIC NORTHWEST CANCER FOUND.
                                                                                                                                                                                                               Holmes EH, Sherwood AL;
                                                                                                                                                                                                                                                   WPI; 2000-687262/67.
N-PSDB; AAC67966.
                WO200064464-A1
                                                                                             23-APR-1999;
                                                      02-NOV-2000
δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     m
                                                                                                                                                                                                   (alphair2Fuct) enzyme and its corresponding nucleic acid. This nucleic acid is specific for a carbohydrate molety found in ganglioside GM1, a terminal galactose betal-3N-acetylgalactosanhae (albetal-3GalNAc) saccharide. Alphai-2Fuct DNA is useful for producing rat alphai-2Fuct DNA is useful for producing rat alphai-2Fuct DNA is useful for producing rat alphai-2Fuct protein by recombinant techniques. Alphai-2Fuct DNA is useful for the preparative synthesis of fucosyl containing glycolipids, glycoroteins, Alphai-2Fuct DNA is useful for detecting oncogenic transformation which alphai-2Fuct is activated in cell transformation, antisense sequences derived from alphai-2Fuct DNA are useful for inhibiting, supressing or treating cancer. Alphai-2Fuct DNA is useful in gene therapy and antisense therapy. The present sequence is rat hepatoma H35 cell
                                                                 Rat hepatoma H35 cell alphal-2fucosyltransferase, useful for producing GM1-specific alphal-2fucosyltransferase enzyme by recombinant techniques and for detecting oncogenic transformation of test tissues .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STSKALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRI 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RDSEQHGNGELRGMFTINSIGRLGNQMGEYATLFALARMNGRLAFIPASMHNALAPIFRI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MLVVQMPFSFPWAHFILFVFTVSTIFHVQQRLAKIQAM--WELPV------QIPVLA 49
                                                                                                                                                                                  The invention relates to rat GM1-specific alpha1-2fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 TLPVLHSATASRIPWQNYHLNDWMEEEYRHIPPGEXVRFTGYPCSWTFYHHLRQEILQEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WFRARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 TLHDHVREEAQKFLRGLQVNGSRPGTFVGYHVRRGDYVHVMPKVWKGVVADRRYLQQALD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 MFRARYSSPVFVVISNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLIQCNHTIMTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTFGIWAAYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLK 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1475; DB 23; Length 380;
Pred. No. 1.1e-146;
30; Mismatches 37; Indels 12
                                                                                                                                              Claim 3; Fig 5; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.78;
77.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 77.7 Matches 275; Conservative
        WPI; 2002-121132/16.
N-PSDB; AAD27207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   380 AA;
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The present sequence is given in a specification relating to a rat ganglioside GM_1-specific alphal-Zfucosyltransferase protein. The protein or its cellular fraction is useful for synthesis of a molecule comprising Fucalphal-ZGalbetal-3GalNac, a glycolipid, glycoprotein, glycolipid or a free oligosaccharide comprising Fucalphal-ZGalbetal-3GalNac. The method involves contacting alphal-2fucosyltransferase with GDP-fucose and a molecule or glycolipid, glycoptotein, glycolipoprotein or oligosaccharide having a terminal Galbetal-3GalNac group. It is also oligosaccharide having a terminal Galbetal-3GalNac group. It is also beligosaccharide having a terminal Galbetal-3GalNac group. It is also beligosaccharide and ganglioside GMLI. The obtained glycoproteins, glycolipids and oligosaccharides are useful as nutritional compositions and fucosyl-GMLI is useful for inducing an nutritional compositions and fucosyl-GMLI is useful for inducing an neurological disease or small cell lung carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         m
New rat ganglioside GMI-specific alphal-2Fucosyltransferase, useful for preparation of fucosyl GMI which is useful as a nutritional composition or immunotherapeutic for cancer and neurological diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATASRIPWQNYHLNDWMEEE 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 VQQRLAKIQAM--WELPV-----QIPVLASTSKALGPSQLRGMWTINAIGRLGNQM 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIFVVTSNGMAWCRENIDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 VGVHVRRGDYVHVMPNVWKGVVADRGYLEKALDMFRARYSSPVFVVTSNGMAWCRENINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLTGGDTIYLANYTLPDSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHDHVREEAQKFLRGLQVNGSRPGTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74.4%; Score 1376; DB 21;
78.9%; Pred. No. 2.7e-136;
live 26; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE16623 standard; Protein; 353 AA.
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                                                                                                                          Claim 2; Fig 3A; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 78.9
Matches 258; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      353 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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YRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHDHVREEAQKFLRGLQVNGSRPGTF VGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIFVVTSNGMAWCRENIDT SHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLTGGDTIYLANYTLPDSP 240 SRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIYLANYTLPDSP 299

257

FLKIFKPEAAFLPEWTGIAADLSPLLK 343 300 FLKVFKPEAAFLPEWVGIPADLSPLLK 326

317

/note= "N-glycosylated" 'note= "N-glycosylated" /note= "N-glycosylated"

/note= "N-glycosylated"

Location/Qualifiers

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Rat hepatoma H35 cell alphal-2fucosyltransferase, useful for producing GMI-specific alphal-2fucosyltransferase enzyme by recombinant techniques and for detecting oncogenic transformation of test tissues .
                                               Rat: alphal-2fucosyltransferase; alphal-2FucT; antisense therapy; galactose betal-3N-acetylgalactosamine; Galbetal-3GalNAc; glycolipid; glycoprotein; glycolipoprotein; oligosaccharide; fucosyl-GMI; cancer; gene therapy; oncogenic transformation; cytostatic; ganglioside; GMI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention relates to rat GM1-specific alphal-2fucosyltransferase
                             H35 cell alphal-2FucT catalytic domain.
                                                                                       cell transformation; catalytic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Fig 3; 41pp; English
          (first entry)
                                                                                                                                                                                                                                                                                                                                 (NWHO-) NORTHWEST HOSPITAL
                                                                                                                                                                                                                                                                                                                                                     Holmes EH, Sherwood AL;
                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-121132/16.
N-PSDB; AAD27208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                           Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           353 AA;
                                                                                                                               Key
Modified-site
                                                                                                                                                                              Modified-site
                             Rat hepatoma
                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                           23-APR-1999;
                                                                                                                                                                                                                                                    JS6329170-B1
                                                                                                                                                                                                                                                                                                              23-APR-1999;
          09-APR-2002
                                                                                                                                                                                                                                                                       11-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Sim
tes 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                            Region
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99US-0298B86

present sequence represents swine alpha(1,2) fucosyltransferase 58.5%; Score 1081.5; DB 20; Length 365; 65.5%; Pred. No. 3.3e-105; 1ve 30; Mismatches 66; Indels 11; Identifying swine genetically resistant to E. coli associated diseases. using PCR-RFUP to assay for polymorphisms in the diseases – using PCR-RFLP to assay fo alpha(1,2) fucosyltransferase 1 gene Disclosure; Fig 1; 19pp; English. Query Match 58.5 Best Local Similarity 65.5 Matches 203; Conservative 365 AA; also be used Seguence 'n 77 GEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATASRIPWQNYHLNDWMEEE 136 9

WPI; 1999-131692/11. N-PSDB; AAX15872. (alphai.2FucT) regress and its corresponding nucleic acid. This nucleic acid is specific for a carbohydrate molety found in ganglioside GM1, a carbohydrate molety found in ganglioside GM1, a terminal galactose betal-3Nacetylgalactosamine (Galbetal-3GalNac) saccharide. Alphai-2FucT DNA is useful for producing rat alphai-2FucT DNA is useful for producing rat alphai-2FucT proprietin by recombinant techniques. Alphai-2FucT DNA is useful for the preparative synthesis of fucosyl containing glycolipids, glycoproteins, glycolipids, glycolopids, glycolipids, glycolipids, glycolipids, glycolipids, glycolipids, glycolipids, glycolipids assaying for changes in expression of alphai-2FucT since alphai-2FucT DNA are useful for inhibiting, suppressing derived from alphai-2FucT DNA are useful for inhibiting, suppressing antisense therapy. The present sequence is rat hepatoma H35 cell alphai-2FucT catalytic domain. 28 VQQRLAKIQAM--WELPV-----QIPVLASTSKALGPSQLRGMWTINAIGRLGNQM 76 Length 353; Indels 74.4%; Score 1376; DB 23; 78.9%; Pred. No. 2.7e-136; Mismatches

26;

Conservative

Matches

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Swine alpha(1,2)fucosyltransferase, FUT1, Escherichia coli, resistant, E. coli-associated intestinal disorder, E coli infection. (BIOT-) BIOTECHNOLOGY RES & DEV CORP. 98WO-US10259 97US-0047181 WO9853101-A2 20-MAY-1998; 20-MAY-1997; Bosworth BT; 26-NOV-1998 Synthetic. Sus sp.

Swine alpha(1,2) fucosyltransferase.

13-MAY-1999

AAW97356;

AA

AAW97356 standard; Protein; 365

RESULT 9

(FUT1). The specification describes methods relating to Escherichia coli-resistant swine. One of the methods for identifying a swine resistant to E. coli-associated intestinal disorders, comprises determining whether the base at 307 of alpha(1,2) fucosyltransferasel gene (FUT1) is adenine (sic), in which case the swine are resistant. The porcine FUT1 polymorphisms can be used to develop drugs for the treatment of swine having E. coli-associated disease. The methods can in breeding programmes to identify swine with resistance

11; Gaps

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A method has been developed for the identification of swine that are resistant to intestinal colonisation by E. coli. The method comprises determining whether a genetic polymorphism associated with resistance to colonisation is present in a swine sample, and then inferring that the swine is resistant if it is homozygous for the polymorphism. The method uses the swine alpha-1,2-fucosyltransferase (FUTI) polymorphism. The present sequence represents swine FUTI. The method enables the breeding
                            51 PVAIFCLAGTPVHPNASDSCPKHPASFSGTWTIYPDGRFGNOMGOYATLLALAQLNGROA 110
                                                                                   PAKDFALLTQCNHTIMTIGTFGIWAAYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEW 331
                                                                                                                                                ||||:||||:|| ||||||||:|| SWIFFHHLREQIRSEFTLADHLRQEAQGVLSGFRLPRIGDRPSTFVGVHVRRGDYLRVMP
                                                                                                                                                                                                             PVQIPVLAST-----SKALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPA
                                                             94 FIPAQMHSTLAPIFRITLPVLHSATASRIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPC
                                                                                                                             SWIFYHHLRQEILQEFTLHDHVREEAQKFLRGLQV--NGSRPGTFVGVHVRRGDYVHVMP
                                                                                                                                                                                            212 KVWKGVVADRRYLQQALDWFRARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New method of identifying swine that are resistant to intestinal colonisation by Escherichia coli - comprises use of genetic polywnorphic markers, used for breeding swine resistant to Escherichia coli-related diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Swine, piq, alpha-1,2-fucosyltransferase 1, FUT1; resistance;
Escherichia coli, infection; oedema; postweaning diarrhoea;
intestinal disorder; polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Swine alpha-1,2-fucosyltransferase 1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SWIE-) SWISS FEDERAL INST TECHNOLOGY ZURICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BIOT-) BIOTECHNOLOGY RES & DEV CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW30630 standard; Protein; 365 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0047181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vogeli P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-059746/05.
                                                                                                                                                                                                                                                                                                                            TGIAADLSPL 341
                                                                                                                                                                                                                                                                                                                                                       350 VGINADLSPL 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB: AAX03811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bosworth BT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW30630;
42
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of swine that are resistant to E. coll-related diseases. This method general polymorphism in the FUTI gene. More particularly, the identification method identifies swine that are resistant to E. coll-related intestinal disorders if, in a sample are resistant to E. coll-related intestinal disorders if, in a sample Larken, the only nitrogen base at residue 307 in the FUTI gene is adenine. Larger amplified fragments from the assay can be used for RFLP analysis, and the assay itself is used as a basis for a kit, applied to swine of any age, in detecting polymorphisms associated with E. coll FIB.

Teceptors. The polymorphisms are useful in developing drugs to treat swine with E. coll-related diseases. However, a mutated form of the portine FUTI gene may interfere with the normal enzyme and prevent it from producing the intestinal receptor for FIB. The detection and treatment of E. coll-related intestinal diseases in swine, where there has been as the detection and the man and a server and a season of the coll-related intestinal diseases in swine, where there has been as the detection and the man and a season a season and a season and a season and a season and a season a seas
                                                                                                                                                                                                                                                                                                                                                                                         has been no success using antibiotics due to unsuccessful prophylaxis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVAIFCLAGTPVHPNASDSCPKHPASFSGTWTIYPDGRFGNOMGQYATLLALAQLNGRQA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 PVQIPVLAST-----SKALGPSQLRGMWTINAIGRLGNQMGEXATLYALAKMNGRPA 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FIPAQMHSTLAPIFRITLPVLHSATASRIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               272 PAKDFALLTQCNHTIMTIGTFGIWAAYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIQPAMHAVLAPVERITLEVLAPEVDRHAPWRELELHDWMSEDYAHLKE-PWLKLIGFPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 SWTFFHHLREQIRSEFTLHDHLRQEAQGVLSQFRLPRTGDRPSTFVGVHVRRGDYLRVMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212 KVWKGVVADRRYLQQALDWFRARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWIFYHHLROEILQEFILHDHVREEAQKFLRGLQV - - NGSRPGTFVGVHVRRGDYVHVMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.5%; Score 1081.5; DB 20; Length 365; 65.5%; Pred. No. 3.3e-105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDP-Fuc:beta-D-galactoside alpha(1,2)-fucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR13751 standard; Protein; 365 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91WO-US00899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Lccal Similarity 65.5
Matches 203; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                350 VGINADLSPL 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             332 TGIAADLSPL 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-NOV-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR13751;
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27-FEB-1996
                                           Pierce JM,
                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                         genome
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                                                                                                                                                                                                                                                                                       54 ALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPV 113
                                                                                                                                                                                                                                                                                                  114 LHSATASRIPWQNYHLNDWMEEEYRHIPPGEYVRFTGXPCSWTFYHHLRQEILQEFTLHD 173
                                                                                                                                                                                                                                                                                                                                               LAPEVDSRTPWRELQLHDWMSEEYADL-RDFLKLSGFPCSWTFFHHLREQIRREFTLHD 189
                                                                                                                                                                                                                                                                                                                                                                                 308
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                    --ASTSK 53
                                                                                                       The amino acid sequence codes for a protein capable of functioning as a GDP- Fuc: Deta-D-Gal alpha(1.2)- fucosyltransferase. The functional protein is represented by amino acids 33 to 365. The enzyme produced by the DNA sequence can be used in enzymatic fucosylation of chain-terminating galactose residues on lactoseramine or neolacto type beta-D-galactoside to aipha-2-L-fucose residues. See also AAR13749-R13752.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDP-L-fucose-beta-D-galactoside 2-alpha-fucosyl-transferase; Fuc-T; synthesis; 2'-fucosyllactose; oligosaccharide; human milk; non-human transgenic mammal; secondary gene product.
                                                                                                                                                                                                                                                               174 HVREEAQKFLRGLQV--NGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWF
                                                                                                                                                                                                                                                                                                                                                                                                           RARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDP-L-fucose-beta-D-galactosidase alpha-1,2-fucosyltransferase
                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                            DB 12; Length 365;
                                               gene conveying post-translational characteristic sence of soluble or membrane bound oligo or de or glycosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGIWAAYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPL 341
                                                                                                                                                                                                                               79; Indels
                                                                                                                                                                                                                                                 12 MAHFILFVFTVSTIFHVQQR-----LAKIQAMWELPVQIPVL----
                                                                                                                                                                                                                    Pred. No. 4.2e-105;
1; Mismatches 79;
                                                                                                                                                                                                           58.4%; Score 1080.5; 59.7%; Pred. No. 4.2e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA.
                                                                                        English
                                                                                                                                                                                                                              41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR80154 standard; Protein; 365
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                                                                                     Disclosure; Fig 3; 155pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                              Conservative
               WPI; 1991-267151/36.
P-PSDB; AAR13751.
                                                                                                                                                                                                                   Similarity
                                                         e.g. the presence
polysaccharide or
                                                                                                                                                                                      365 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-SEP-1995
                                                                                                                                                                                                                             209;
                                               Isolation
                                                                                                                                                                                       Sequence
                                                                                                                                                                                                         Query Match
Best Local 9
Lowe JB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR80154
                                                                                                                                                                                                                    Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                  131
                                                                                                                                                                                                                                                                                                                                                                                        190
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AAR80154
Dp
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is encoded by CDNA (AAQ99461) isolated from a human epidermal carcinome cell line. The enzyme is responsible for the synthesis of 2'-fucosyllactose, one of the oligosaccharides in human milk. Other products of Fuc-T include glycoprotiens contq. beta-linked terminal galactose residues which can be fucosylated by Fuc-T. This DNA can be used to produce non-human transgenic mammals able to produce secondary gene products, e.g. oligosaccharides, in their milk. The transgenic mammals milk biochemically resembles human milk. This humanised milk can be used in the prepn. of an enteral nutritional product useful in the nutritive maintenance of an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 ALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---LAKIQAMWELPVQIPVL-----ASTSK 53
                                                                                                                                                                                                                                Prodn. of human:ised milk by non-human transgenic mammal - by inserting heterologous gene encoding human catalytic entity which produces oligo:saccharide(s) and glyco:conjugate(s) into mammal's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 LAFLLVCVLSVIFFLHIHQDSFPHGLGLSILCPDRRLVTPPVAIFCLPGTAMGPNASSSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 LHSATASRIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDP-L-fucose-beta-D-galactoside 2-alpha-fucosyltransferase; glycosyltransferase; glycosylation; oligosaccharide; glycoprotein; glycolipid; transgenic animal; cattle; milk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 HVREEAQKFLRGLQV--NGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.4%; Score 1080.5; DB 16; Length 365; 59.7%; Pred. No. 4.2e-105;
                                                                                                                                                                                                                                                                                                                                                                                                                                          GDP-L-fucose-beta-D-galactoside 2-alpha-fucosyl-transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292 FGIWAAYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPL 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79; Indels
                                                                Mukerji P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41; Mismatches
                                                             C, Moreman KW,
Smith DF;
                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 62-64; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 MAHFILFVFTVSTIFHVQQR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR70422 standard; Protein; 365
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                                                          Kopchik JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                     Prieto PA,
                                                                                                                                                WPI; 1995-336739/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
(ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity
Matches 209; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     365 AA;
                                                                                                                                                                           N-PSDB; AAQ98461
                                                             Cummings RD,
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08-APR-1996
                                                 14-SEP-1995
                                                                                                                                           Pierce JM,
                                                                                                                               Cummings
                                                                                                                                                                                                                                                                                                                            Seguence
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                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                            54 ALGPSQLRGMWTINAIGRLGNOMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPV 113
                                                                                                                                                                                                                                                                                                                                                                                                       114 LHSATASRIPWQNYHLNDWMEEEYRHIPPGGYVRFTGYPCSWTFYHHLRQEILQEFTLHD 173
                                                                                                                                                                                                                                                                                                                                                                                                                                             231
                                                                                                                                                                                New transgenic non-human mammal milk prods - contg. heterologous components produced as secondary gene prods. of an heterologous gene
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                     12 MAHFILEVFIVSTIFHVQQR-----LAKIQAMWELPVQIPVL-----ASTSK 53
                                                                                                                                                                                                                                                                                                                                                                        11 LAFLLVCVLSVIFFLHIHQDSFPHGLGLSILCPDRRLVTPPVAIFCLPGTAMGPNASSSC 70
                                                                                                                                                                                                                              2-Alpha-fucosyltransferase (AAR70422) is encoded by a cDNA clone (AAR701083) isolated from a human epidermal carcinoma A431 library. The enzyme can be expressed in the milk of a transgenic mammal, esp. cow. This allows large-scale prodn. of oligosaccharides and glycosylated proteins and lipids in the milk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HVREEAQKFLRGLQV -- NGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGT
                                                                                                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                            58.4%; Score 1080.5; DB 16; Length 365; 59.7%; Pred. No. 4.2e-105; Live 41; Mismatches 79; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDP-L-fucose-beta-D-galactoside 2-alpha-fucosyltransferase; glycosyltransferase; oligosaccharide; glycoprotein; glycolipid; transgenic animal; cattle; glycosylation; milk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FGIWAAYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPL 341
                                                                                                                      Mukerji
                                                                                                                    , Moremen KW,
Smith DF;
                                                                                                                                                                                                           Example 1; Page 62-64; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein; 365
                                                         95WO-US00967
                                                                             94US-0208889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2-Alpha-fucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                      JJ,
                                                                                                                                                                                                                                                                                                                      Best Local Similarity 59.7
Matches 209; Conservative
                                                                                                                   , Kopchik
Prieto PA,
                                                                                                                                                WPI; 1995-328284/42.
N-PSDB; AAT01083.
                                                                                                ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR70421 standard;
                                                                                                                                                                                                                                                                                          365 AA;
                                                                                                                    RD,
Homo sapiens
                                                         24-JAN-1995;
                                                                             09-MAR-1994;
                 W09524495-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-FEB-1996
                                     14-SEP-1995
                                                                                                                             Pierce JM,
                                                                                                                      Cummings
                                                                                                                                                                                                                                                                                            Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR70421;
                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                      131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174
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q
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                                                                                                                                                                                                                                                                                                                                                                                            Q\underline{Y}
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54 ALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPV 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGT 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 LAFLLVCVLSVIFFLHIHQDSFPHGLGLSILCPDRRLVTPPVAIFCLPGTAMGPNASSSC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alpha-1,2-fucosyltransferase (AAR70421) is encoded by a cDNA clone (AAT01082) isolated from a human epidermal carcinoma cell line A431 cDNA library. The enzyme can be expressed in the milk of a transgenic mammal, esp. cow. This allows large-scale prodn oligosaccharides or glycosylated proteins and lipids in the milk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 MAHFILFVFTVSTIFHVQQR------LAKIQAMWELPVQIPVL-----ASTSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 HVREEAQKFIRGLQV--NGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.4%; Score 1080.5; DB 16; Length 365; 59.7%; Pred. No. 4.2e-105;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Transgenic animal expressing heterologous catalyst - used in metabolite prodn esp. glycosyltransferase for prodn. of oligosaccharide(s) and glyco-conjugate(s) in the milk, useful foods, pharmaceuticals, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FGIWAAYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPL 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---
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D
                                                                                                                                                                                                                                                                                               Mukerji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41; Mismatches
                                                                                                                                                                                                                                                                                             Kopchik JJ, Moremen KW, neto PA, Smith DF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 62-64; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA.
                                                                                                                                            95WO-US01147.
                                                                                                                                                                                             94US-0209132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR90572 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                       Prieto PA,
                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-328279/42.
N-PSDB; AAT01082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human H-transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 209; Conserv
                                                                                                                                                                                                                                              (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          365 AA;
Homo sapiens
                                         WO9524488-A1
                                                                                                                                              24-JAN-1995;
                                                                                                                                                                                               09-MAR-1994;
                                                                                                                                                                                                                                                                                               RD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 ALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 LHSATASRIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHD 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HVREEAQKFLRGLQV--NGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWF 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGT 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 MAHFILFVFTVSTIFHVQQR------LAKIQAMWELPVQIPVL-----ASTSK 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Redn. of rejection of xenogeneic cells following transplantation by introducing a vector expressing fucosyl:transferase into the cells
H-transferase; xenograft hyperacute rejection; transplantation; glycosyltransferase; galactose alpha(1,3) galactose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 17; Length 365;
                                                                                                                                                                                                                                                 Squinto SP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.4%; Score 1080.5; DB 17; Lengtl
59.7%; Pred. No. 4.2e-105;
Live 41; Mismatches 79; Indels
                                                                                                                                                                                                                                                 Sandrin MS,
                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 45-47; 69pp; English.
                                                                                                                                                                                                                                                 Rother RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: May 27, 2003, 15:06:17 Job time: 44.6293 secs
                                                                                                                                                          94US-0278282.
94US-0260201.
                                                                                                                                95WO-US07554
                                                                                                                                                                                                   (ALEX-) ALEXION PHARM INC. (AUST-) AUSTIN RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 59.79
Matches 209; Conservative
                                                                                                                                                                                                                                                 Mckenzie IFC,
                                                                                                                                                                                                                                                                          WPI; 1996-049326/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           365 AA;
                                                                                                                                                                                                                                                                                        N-PSDB; AAT12238
                                           Homo sapiens
                                                                       WO9534202-A1
                                                                                                                                                          21-JUL-1994;
15-JUN-1994;
                                                                                                                             14-JUN-1995;
                                                                                                    21-DEC-1995
                                                                                                                                                                                                                                              Fodor WL,
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RESULT 2
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1850
I MLVVQMPFSFPWAHFILFVF......AAFLPEWTGIAADLSPLLKH 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, 7, 8 Sequence 8, 7, 8 Sequence 7, 8 Sequence 10, 8 Sequence 11, 8 Sequence 6, 8 Sequence 10, 8 Sequence 
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2: /cgn2_6/ptodata/l/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/l/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/l/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/l/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/l/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-254-077A-8
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US-09-298-886-10
US-09-298-886-10
US-09-298-886-10
US-09-294-077A-12
US-08-394-06
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US-09-151-592-2
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US-08-395-800A-2
US-09-435-800A-3
US-09-43-598-2
US-09-390-131-5
US-08-913-805A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                                                                                                                                  - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                         May 27, 2003, 15:03:22
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28 92 5.0 575 39 90 4.9 575 31 87.5 4.7 365 33 87.5 4.7 365 34 87.5 4.7 365 35 82.5 4.7 365 36 82.5 4.5 183 37 82.5 4.5 183 38 82.5 4.5 183 39 82.5 4.5 183 39 82.5 4.5 183 39 82.5 4.5 183 39 82.5 4.5 183 39 82.5 4.5 183 39 82.5 4.5 183 39 82.5 4.5 183 39 82.5 4.5 183 39 82.5 4.5 183 39 82.5 4.5 183 39 82.5 4.5 183 39 82.5 4.5 183 39 82.5 4.5 183 44 81.5 4.4 630 42 81.5 4.4 630 43 604 44 81.5 4.4 630 42 81.5 4.4 630 43 604 44 80 4.3 604 45 80.5 290 80.5 290 80.5 290 80.6 20 80.6 11 80.6 20 80.6 11 80.6 20 80.6 11 80.6 20 80.6 11 80.6 20 80.6 11 80.6 20 80.6 11 80.6 20 80.6 11 80.6 20 80.6 11 80.6 20 80.6 11 80.6 20 80.6 11 80.6 20 80.6 11 80.6 20 80.6 11 80.6 20 80.6 11 80.6 20 80.6 11 80.6 20 80.6 11 80.6 20	09 - 442 - 629 - 2 08 - 913 805A-1 08 - 978 - 741 - 2 09 - 933 729A-3 08 - 938 729A-3 08 - 538 055-3 08 - 539 055-3 09 - 280 587-3 09 - 280 598-3 09 - 280 598-3 00 - 959 - 943-7 07 - 959 - 959 - 959 - 959 - 959 - 959 - 959 - 959 - 959 - 959 - 959 - 959 - 959 - 959 - 959 - 959 - 959 - 959	298886 al. CIDS AND PROT FIC ALPHA1-2 S/09/296,886 26	; Score 1850; DB 4; ; Pred. No. 4.9e-204 0; Mismatches 0;	FHVQQRLAKIQAMWEL 	YALAKMNGRPAFIPAQMHSTLA 	SEYVRFTGYPC 	RGDYVHVMPKVWKGVVADRRYL RGDYVHVMPKVWKGVVADRRYL	PAGDGIEGSPAKDFALLTQCNH 	PLLKH PLLKH
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SAME, METHOD FOR PRODUCING THE SAME AND A METHOD OF
GENOTYPING A PERSON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 343;
                                                                                                                                                                                                                                       ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRBNY APPLICATION DATA:
APPLICATION NUMBER: US/08/395,800A FILING DATE: 28-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.1%; Score 1832.5; DB ilarity 99.7%; Pred. No. 5e-202; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                  Sequence 8, Application US/08395800A
Patent No. 5807732
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
TELEBRORE: (703) 413-220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 8:
                                                                         APPLICANT: LENNON, GREGORY
APPLICANT: ROUGUIER, SYLVIE
APPLICANT: GTORGI, DOMINTOUE
APPLICANT: GTORGI, DOMINTOUE
TITLE OF INVENTION: GDP-L-FUCOS
TITLE OF INVENTION: 2-ALPHA-L-I
TITLE OF INVENTION: GROUTPING
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 343 amino acids
amino acid
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                                              GENERAL INFORMATION:
APPLICANT: LOWE,
                                                                                                                                                                                                                                                                       CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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RESULT 3 US-09-254-077A-8

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patent No. 6399758
GENERAL INFORMATION:
APPLICANT: SANDRIN, MAURO S.
APPLICANT: MCKERZIE, IAN C. F.
TITLE OF INVENTION:
FILE REFERENCE: 30562.505W0
CURRENT APPLICATION NUMBER: US/09/254,077A
CURRENT FILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: PCT/AU97/00540
PRIOR PELING DATE: 1997-08-22
PRIOR FILING DATE: 1997-08-22
PRIOR FILING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: MCKBRIZIE, IAN C. F.
TITLE OF INVENTION: NUCLEIC ACIDS FOR REDÜCING CARBOHYDRATE EPITOPES
FILE REFERENCE: 30562.50SWO
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Pred. No. 5e-202;
0; Mismatches 0;
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CURRENT FILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: PCT/AU97/00540
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: PCT/AU97/00540
PRIOR APPLICATION NUMBER: PO 1823
PRIOR FILING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 12
SOGTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 340
8, Application US/09254077A
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99.78;
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Best Local Similarity 99.7
Matches 343; Conservative
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US-09-254-077A-8
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US-09-254-077A-6
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VVSSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTVMTIGTFGIWAAYLA 296
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APPLICANT: ELIC H. HOLMES et al.

TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE
TITLE OF INVENTION: GMI-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: SANDRIN, MAURO S.
APPLICANT: MACKENZIE, IAN C. F.
TITLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRAFE SPLTOPES
FILE REFERENCE: 30562.5USWO
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       81.6%; Score 1509.5; DB 4; Length 347; 81.3%; Pred. No. 6.9e-165; ive 18; Mismatches 42; Indels 5;
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CURRENT PILING DATE: 1999-06-11
PRIOR PRILING DATE: 1997-06-22
PRIOR FILING DATE: 1997-08-22
PRIOR FILING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 9
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CURRENT FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 29
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Matches 283; Conservative
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ORGANISM: Lepus Sp.
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                                                                                                                                        1 MLVVQMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAMWELPVQIPVLASTSKALGPSQL 60
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APPLICANT: SANDRIN, MAURO S.
APPLICANT: SANDRIN, MAURO S.
APPLICANT: SANDRIN, MAURO S.
TITLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES
FILE REFERENCE: 30562.5USWO
CURRENT APPLICATION NUMBER: US/09/254,077A
CURRENT FILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: PCT/AU97/00540
PRIOR FILING DATE: 1997-08-22
PRIOR FILING DATE: 1997-08-23
PRIOR FILING DATE: 1996-08-23
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       Length 340;
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       DB 4;
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Pred. No. 5e-167;
1; Mismatches 34
82.6%; Score 1528; DB 4
82.0%; Pred. No. 5e-167;
tive 24; Mismatches 3
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82.0%; Pred
tive 24; J
                                                                      Matches 282; Conservative
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Best Local Similarity
                                          Similarity
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       Query Match
Best Local 3
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                                                                                                                    Sequence 6, Application US/07914281
Patent No. 5324663
                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lepus Sp
                                                                                                                                                                        RESULT 9
US-09-254-077A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Lep
US-09-254-077A-12
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                                                                                                                                                                                                                                                                                                                                 170 TLHDHVREEAQKFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALD 229
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                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Eric H. Holmes et al.

TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAI GANGLIOSIDE
TITLE OF INVENTION: GMI-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERASE AND USES
FILE OF INVENTION: FIBEROF
FILE REFERENCE: 8511-029
                                                                                                                                                                                                                 50 STSKALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 TLPVLHSATASRIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEF
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                                                                                                                                                                                                                                                                                                                                                                                                          240 MFRARYSSPVEVUTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTI
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                                                                                                                             12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.4%; Score 1376; DB 4; Length 353; 78.9%; Pred. No. 1.6e-149;
                                                                                                                             Indels
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                                                                                                                                                         1 MLVVQMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAM--WELPV----
                                                                                                 ; Score 1475; DB 4;
; Pred. No. 7.4e-161;
30; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/298,886
CURRENT FILING DATE: 1999-04-26
NUMBER OF SEQ ID NGS: 29
SOTTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/09298886
Patent No. 6329170
                                                                                                 79.78;
                                                        Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Rattus norvegicus
                                                                                                             Best Local Similarity 77.7 Matches 275; Conservative
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SOFTWARE: Patentin
SEQ ID NO 8
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                           380
                                                                  US-09-298-886-8
                                        TYPE: PRT
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                                                                                                  Query Match
                                                      ORGANISM:
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                           LENGTH:
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GENERAL INFORMATION:
APPLICANT: LOWE, JOHN B.
APPLICANT: LOWE, JOHN B.
TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
                              SHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLTGGDTIYLANYTLPDSP 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 LPVQIPVLASTSKALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMH 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOR REDUCING CARBOHYDRATE EPITOPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STLAPIFRITLPVLHSATASRIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHH
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                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/09254077A
Patent No. 639978
GENERAL INFORMATION:
APPLICANT: SAURRIN, MAURO S.
TITLE OF INVENTION: NOCLEIC ACIDS FOR REDUCING FILE REPRENCE: 30562.5000
CURRENT APPLICATION NUMBER: US/09/254,077A
CURRENT FILING DATE: 1999-06-11
PRIOR FILING DATE: 1997-08-22
PRIOR FILING DATE: 1997-08-22
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Sequence 1, Application US/08273411
Patent No. 5625124
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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Best Local Similarity
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US-08-273-411-1
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TITLE OF INVENTION: OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
TITLE OF INVENTION: GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
   SEQUENCES THAT DETERMINE THESE STRUCTU
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                                                  OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
                                    AUDRESSEE: P.C. STREET: 1755 Jefferson Davis Highway, Fourth Floor CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                              Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41; Mismatches
                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye, Jean-Paul M. P.
NEGISTRATION NUMBER: 21,451
REFERENCE/DOCKET NUMBER: 2363-060-55
     OF CLONED GENETIC
                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/914,281
                                                                                                                                                                                                               PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-393-246-6
; Sequence 6, Application US/08393246
; Patent No. 5595900
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LOWE, JOHN B.
                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (703)521-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 365 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
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     TITLE OF INVENTION: OF NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
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                                                                                                                                    U.S.A.
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                                                                                                                                                22202
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                                                                                                                                COUNTRY:
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Best Local
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OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HVREEAQKFLRGLQV--NGSRPGTFVGVHVRRGDYVHVMPKVWKGYVADRRYLQQALDWF
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                                                      MAIER & NEUSTADT,
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                                                                                         Fourth Floor
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Pred. No. 1.5e-115;
                                                                                                                                                                                                                                                                 Patentin Release #1.0, Version #1.25
                           CLIY: ALINGTON SPIVAK, MCCLELLAND, M. STREET: 1755 Jefferson Davis Highway, Fot CLIY: Arlington STATE: Virginia COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55
                                                                                                                                                                                                                                                                                                                                                                              US 08/220,433
                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 30-MAR-1994
APPLICATION NUMBER: US 07/914,281
FILING DATE: 20-JUL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,24'
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Lavalleye, Jean-Paul M. P.
                                                                                                                                                                                                                        IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFRA: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 6:
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59.7%;
                                                                                                                                                                                                          Floppy disk
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METHODS AND PRODUCTS FOR THE SYNTHESIS OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS, GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
                    54 ALGPSQLRGHWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LHSATASRIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHD 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGT 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 HLREBAQSVLGQLRLGRTGDRPRTFVGVHVRRGDYLQVMPQRWKGVVGDSAYLRQAMDWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 HVREEAQKFLRGLQV--NGSRPGTFVGVHVRRGDYVHVMPKVWRGVVADRRYLQQALDWF
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1755 Jefferson Davis Highway, Fourth Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.4%; Score 1080.5; DB 1; Length 365; 59.7%; Pred. No. 1.5e-115; Live 41; Mismatches 79; Indels 21;
                                                                    292 FGIWAAYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPL 341
                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILLOATION NUMBER: US/08/525,058A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 2363-060-55
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Lavalleye, Jean-Paul M. P. REGISTRATION NUMBER: 31,451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                 Sequence 6, Application US/08525058A
Patent No. 5770420
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ZIP: 22202
COMPUTER READABLE FORM:
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(703)486-2347
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TITLE OF INVENTION: OF C
TITLE OF INVENTION: GLY
TITLE OF INVENTION: OF C
TITLE OF INVENTION: OF C
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                        JOHN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 248855 OPAT URINFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Arlington
STATE: Virginia
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                                                                                                                                                                              US-08-525-058A-6
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Matches 209;
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                                   APPLICANT: Gordon, Jeffrey I.
TITLE OF INVENTION: Animal Model for Gastro-Intestinal
TITLE OF INVENTION: Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1: FROM 1 TO 365
                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 1100 Peachtree Street, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 31,284
REFERENCE/DOCKET NUMBER: W0106
TELEPHONE: (404) 815-6508
TELEPHONE: (404) 815-6555
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/273,411 FILING DATE:
                                                                                                                                                                                                                                                                                            PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                          E: Floppy disk
IBM PC compatible
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LOCATION: 1..365
OTHER INFORMATION: /note=
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Larsen, et al.
Proc. Nat'l Acad.
                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: NO
GENERAL INFORMATION:
APPLICANT: Falk, Per
                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                 COUNTRY: USĀ
ZIP: 30309-4530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209;
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Matches
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2-ALPHA-L-FUCOSYLTRANSFERASES, DNA SEQUENCES ENCODING SAME, METHOD FOR PRODUCING THE SAME AND A METHOD OF GENOTYPING A PERSON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 LHSATASRIPWQNYHENDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHD 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----LAKIQAMWELPVQIPVL-----ASTSK 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 365;
                                                  SEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 ARLINGTON
                    292 FGIWAAYLIGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWIGIAADLSPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/395,800A FILING DATE: 28-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1080.5; DB 1;
Pred. No. 1.5e-115;
41; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                    Sequence 10, Application US/08395800A Patent No. 5807732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
TELECOMMUTICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-220
TELEFAX: 248855 OPATUR
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                   APPLICANT: LENNON, GREGORY
APPLICANT: ROUGUIER, SYLVIE
APPLICANT: GRORGI, DOMINIQUE
APPLICANT: GRORGI, DOMINIQUE
TITLE OF INVENTION: GDP-L-FUCOS
TITLE OF INVENTION: SAME, METH
TITLE OF INVENTION: GENOTYPING
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 MAHFILFVFTVSTIFHVQQR----
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                                                                                                                                                                                                                                                                                                                 LOWE, JOHN B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
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Best Local Similarity
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                                                                                                                                                                                                                                                        Patent No. 5807732
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-395-800A-10
                                                                                                                                                                 RESULT 15
US-08-395-800A-10
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2-ALPHA-L-FUCOSYLTRANSFERASES, DNA SEQUENCES ENCODING THE SAME, METHOD FOR PRODUCING THE SAME AND A METHOD OF GENOTYPING A PERSON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 LAFILIVCVLSVIFFLHIHQDSFPHGLGLSILCPDRRLVTPPVAIFCLPGTAMGPNASSSC 70
250 RARHEAPVFVVISNGMEWCKENIDISQGDVTFAGDGQEATPWKDFALLIQCNHTIMTIGT 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 365;
                                                        292 FGIWAAYLIGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWIGIAADLSPL 341
                                                                                         MCCLELLAND, MAIER & NEUSTADT
DAVIS HIGHWAY, SUITE 400
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PatentIn Release #1.0, Version #1.30
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28-FEB-1995
                                                                                                                                                                                                                                                           Sequence 6, Application US/08395800A
Patent No. 5807732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LOWE, JOHN B
APPLICANT: LENNON, GREGORY
APPLICANT: ROUGUIER, SYLVIE
APPLICANT: GIORGI, DOMINIQUE
APPLICANT: KELLY, ROBERI J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-220
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 6:
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MEDIUM TYPE: Floppy disk
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                              RESULT 14
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Sequence 2, Appli
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Sequence 10, Appl
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Sequence 13, Appl
Sequence 11, Appl
Sequence 1, Appli
Sequence 4, Appli
Sequence 2, Appli
                                                                  May 27, 2003, 15:08:29; Search time 14.8627 Seconds (without alignments) 2295.367 Million cell updates/sec
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1 MLVVQMPFSFPMAHFILFVF.......AAFLPBWTGIAADLSPLLKH 344
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US-10-040-863-11

US-10-940-863-11

US-09-999-672-8

US-10-040-863-8

US-10-040-863-10

US-10-040-863-10

US-10-040-863-10

US-09-844-268-13

US-09-844-268-13

US-09-863-475A-6

US-09-863-475A-6

US-09-88-838-2

US-09-479-614-12

US-09-479-614-12

US-09-479-614-2

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US-09-839-135-10
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                                                                                                                                                                                                    375593 seqs, 99172665 residues
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Maximum Match 1008
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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ALIGNMENTS

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181 KFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIF 240
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                                                      GENERAL INFORMATION:

SENERAL INFORMATION:

TIPLE OF INVENTION:

TITLE OF INVENTION:

GMI-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERASE AND USES

TITLE OF INVENTION:

PRIOR FILING DATE:

PRIOR FILING DATE:

1999-04-26
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              Sequence 11, Application US/0999672 Patent No. US20020127655Al
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US-09-999-672-11
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LENGTH: 344
TYPE: PRT
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US-09-999-672-11
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241 VVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLT 300
                                                                                                                                                        Sequence 11, Application US/10040863
Patent No. US20020137165A1
GENERAL INFORMATION:
APPLICANT: EIC H. Holmes et al.
TITLE OF INVENTION: GMI-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENTION: GMI-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERASE AND USES
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Patent No. US2001005584A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MAURO SERGIO
TITLE OF INVENTION: GLYCOSYLTRANSFERASE
TITLE OF INVENTION: GLYCOSYLTRANSFERASE
FILE REFERENCE: 30562.60SM0
CURRENT APPLICATION NUMBER: US/09/051,034A
PRIOR APPLICATION NUMBER: PCT/AU97/00452
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                                                     301 GGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 344
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Best Local Similarity 100.0%; Pred. No. 9.1e-183;
Matches 344; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                     FILE REFERENCE: 8511-029
CURRENT APPLICATION NUMBER: US/10/040,863
CURRENT FILING DATE: 2001-11-01
                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                        US-10-040-863-11
                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 11
LENGTH: 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                  241 VVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLT 300
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                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/0999672

Sequence 8, Application US/0999672

Patent No. US20020127655al

GENERAL INFORMATION:

APPLICANT: Eric H. Holmes et al.

TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE

TITLE OF INVENTION: GM.-SPECIFIC ALPHA1-2 FUCOSYLTRANSFERASE AND USES

FILE REFERENCE: 6511-029

CURRENT FILING DATE: 2001-10-31

PRIOR APPLICATION NUMBER: US/09/959,672

CURRENT FILING DATE: 2001-10-31

PRIOR PAPLICATION NUMBER: US/09/228,886

PRIOR FILING DATE: 1999-04-26
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                                                                                                                                                                                                                                                         82.6%; Score 1528; DB 10;
82.0%; Pred. No. 1.7e-149;
ative 24; Mismatches 34;
                             60/024,279
                                   JMBEA.
1996-08-21
TIMBER: PO1402
PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: 60/024
PRIOR FILING DATE: 1996-08-21
PRIOR APPLICATION NUMBER: PO1402
PRIOR FILING DATE: 1996-08-02
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VEX: 2.1
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
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TYPE: PRT
ORGANISM: Sus Domesticus
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Matches 282;
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US-09-999-672-8
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SEQ ID NO 2
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                                                              SLPVLHSDTARKIPWQNYHLNDWMEERYRHI-PGHFVRFTGYPCSWTFYHLRPEILKEF 179
WFRARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTI 289
                                                                                                                                                                                                     MFRARYSSPVFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTIMTI 299
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Eric H. Holmes et al.

TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE
TITLE OF INVENTION: GML-SPECIFIC ALPHAl-2 FUCOSYLTRANSFERASE AND USES
TITLE OF INVENTION: THERRORY
FILE REFERENCE: 8511-029
CURRENT APPLICATION NUMBER: US/10/040,863
CURRENT FILING DATE: 1999-04-23
RIGH APPLICATION NUMBER: 09/298,886
PRIOR PILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN Ver. 2.0
                                           TLPVLHSATASRIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEF 169
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                                                                                                                                                                                                                                                                                                                                              Sequence 8. Application US/10040863 Patent No. US20020137165A1
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US-10-040-863-8
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RESULT 6 US-09-999-672-10

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; Sequence 10, Application US/10040863
; Patent No. US20020137165A1
; GENERAL INFORMATION:
; APPLICANT: Eric H. Holmes et al.
; TITLE OF INVENTION: WAL-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERASE AND USES
; TITLE OF INVENTION: THEREOF
                                        GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Eric H. Holmes et al.

TITLE OF INVENTION: WUCLEIC ACIDS AND PROTEINS OF A RAT GANGLIOSIDE

TITLE OF INVENTION: GM.-SPECIFIC ALPHAI-2 FUCOSYLTRANSFERASE AND USES

TITLE OF INVENTION: THEREOF

FILE REPRENCE: 8511-029

CURRENT APPLICATION NUMBER: US/09/999,672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197 VGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIFVVTSNGMAWCRENIDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10;
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CURRENT APPLICATION NUMBER: US/10/040,863
CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: 09/298,886
PRIOR FILING DATE: 1999-04-23
                                                                                                                                                                                        CURRENT FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: US/09/298,886
PRIOR FILING DATE: 1999-04-26
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Sequence 10, Application US/0999672
Patent No. US20020127655A1
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78.98;
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78.98;
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US-09-999-672-10
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SOFTWARE: Patentin Ver.
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Best Local Similarity
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LENGTH: 353
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LENGTH: 353
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QY 332 TGIAADLSPL 341 bb 350 VGINADLSPL 359 RESULT 9 US-09-844-705-13 Sequence 13, Application US/09844705 Patent No. US200201338361 GENERAL INFORMATION: APPLICANT: BOSWORTH, BRAD APPLICANT: WOGELL, PETER TITLE OF INVENTION: METHODS AND COMPOSITIONS TITLE REPERBACE: 21419/90368 CURRENT APPLICATION NUMBER: US/09/844,705 CURRENT FILING DATE: 2001-04-27 CURRENT FILING DATE: 2001-04-27	; FALCH RIGHTON MADEN: US/143,/00 ; MUMBER OF SEQ ID NOS: 13 ; SOFTWARE: Patentin Ver. 2.0 ; ENGTH: 365 ; TIPE: PRT ; CRGANISM: Porcine US-09-844-705-13	Query Matches Matches Matches 4 2 P 4 2 P 5 1 P 5 1 P 6 111 F 7 154 S 7 154 S 7 212 K 7 272 P 6 230 K 7 272 P 7 332 T 6 230 K 7 332 T 7 332 T 8 332 T 9 332 T 7 272 P 7 272 P 8 332 T 8 332 T 9 250 P 9 250 P 1111E OF 111E OF 11IE OF 1IE	; PRIOR FILING DATE: 2001-03-21
Matches 258; Conservative 26; Mismatches 31; Indels 12; Gaps 3; Qy 28 VQORLAKIQAM-WELPVQIPVLASTSKALGPSQLRGMWTINALGERGNO 76 :	QY 257 SHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIMAAYLTGGDTIYLANYTLPDSP 316	RESULT 6 Sequence 13, Application US/09844268 Parten No. US2002019935A1 Sequence 13, Application US/09844268 Parten No. US2002019935A1 Sequence 13, Application US/09844268 Parten No. US2002019935A1 APPLICANT: WOOSTI, PRITE PARTEN NO. US 11, PRITE PARTEN NO. US	

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NS TO IDENTIFY SWINE GENETICALLY DLI ASSOCIATED DISEASES
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|EWCRKNIDTSRGDVIFAGDGREAA 289
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ANFTLPTSSFLKIFKPEAAFLPEW 349
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6e-103;
ss 66; Indels 11; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 LHSATASRIPWQNYHLNDWMEEEFRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHD
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                                                                                                                                                                                                                                                         Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENCODING A CHIMERIC
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                                                                                                                                                                                                                                                       DB 10;
                                                                                                                                                                                                                                                    58.4%; Score 1080.5; DB 1.
59.7%; Pred. No. 3.3e-103;
iive 41; Mismatches 79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MCKENZIE, IAN FARQUHAR CAMPBELL APPLICANT: MCKENZIE, IAN FARQUHAR CAMPBELL APPLICANT: SANDER.N. MAUNO SERGIO TITLE OF INVENTION: IMPROVED NUCLEIC ACIDS ITILE OF INVENTION: GLYCOSYLITRANSFERASE FILE REPERBENCE: 30562.6GNNO CURRENT APPLICATION NUMBER: US/09/051,034A CURRENT FILING DATE: 1998-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT/AU97/00492
                                                                                                                                                                                         9
                                                                                                                          ; TOPOLOGY: unknown; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-863-475A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60/024,279
TELEPHONE: (703)521-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09051034A Patent No. US20010055584A1
                                                                                                      LENGTH: 365 amino acids TYPE: amino acid
                 TELEFAX: (703)486-2347
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JMBER: PO1402
1996-08-02
                                                                                                                                                                                                                                                                                                                                     12 MAHFILFVFTVSTIFHVQQR-----
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                                                                                                                                                                                                                                                                        Local Similarity 59.7%
Les 209; Conservative
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SEQ ID NO 4
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US-09-051-034A-4
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APPLICANT: LOWE, JOHN B.
TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES
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                                                                                                                                                                                                                                                                                                                                                                                                                    114 LHSATASRIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHD 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231
                                                                                                                                                                                                                                                                                                                                     54 ALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPV 113
                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                            11 LAFLLVCVLSVIFFLHIHQDSFPHGLGLSILCPDRRLVTPPVAIFCLPGTAMGPNASSSC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 HVREEAQKFLRGLQV -- NGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
                                                                                                                                                                                                           21;
                                                                                                                                                                   Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310 FGFWAAYLAGGDTVYLANFTLPDSEFLKIFKPEAAFLPEWVGINADLSPL 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292 FGIWAAYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPL 341
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STREET: 1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                    -LAKIQAMWELPVQIPVL-
                                                                                                                                                                   DB 9;
                                                                                                                                                                 58.4%; Score 1080.5; DB 9; 59.7%; Pred. No. 3.3e-103; iive 41; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/863,475P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 07/914,281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 24-May-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/09863475A Patent No. US20020102688A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 20-JUL-1992 ATTORNEY/AGENT INFORMATION:
                     SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                       12 MAHFILFVFTVSTIFHVQQR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Arlington STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                       Best Local Similarity 59.7
Matches 209; Conservative
NUMBER OF SEQ ID NOS: 40
                                                                              TYPE: PRT
CORGANISM: Homo sapiens
US-10-105-963-10
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                                         SEQ ID NO 10
LENGTH: 365
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RESULT 14

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Sequence 14, Application US/09479614
Publication No. US20030013183A1
GENERAL INFORMATION:
APPLICANT: McCall, Catherine
APPLICANT: Weber, Exic
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
FILE REFERENCE: P-1047
CURRENT APPLICATION NUMBER: US/09/479,614
EARLIER APPLICATION NUMBER: 60/115,033
EARLIER FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
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APPLICANT: Weber, Eric
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
FILE REFERENCE: P-1047
CURRENT APPLICATION NUMBER: US/09/479,614
CURRENT FILING DATE: 2000-01-07
EARLIER APPLICATION NUMBER: 60/115,033
EARLIER FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 VSACTMNFIPPTVKLEHSSCNPLGDTG-----STIQLLCLISG---YVPGDMEVTWLVD 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 ---LAPIFRITLPVLHSATASRIPWQNYHLNDWMEBEYRHIPPGEYVRFTGYPCSWTFYH 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 HLRQEILQEFTLHDHVREEAQKFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                199 -----OGFIFEDHARKCTESDPRGVSTYLSPPSPL-----DLYVHKSPKI-TCLVV 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278 LLTQCNHTIMTIGTFGIWAAYLTGGDTIYLANYTLPDSP-----FLKI----FKPEA-A 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09479614 Publication No. US20030013183A1
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Best Local Similarity 23.8
Matches 72; Conservative
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US-09-479-614-14
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160 HLRQEILQEFTLHDHVREEAQKFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVA 219
                                              264 ------QGFTFEDHARKCTESDPRGVSTYLSPPSPL------DLYVHKSPKI-TCLVV 308
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394 FLP 396
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Search completed: May 27, 2003, 15:25:45 Job time : 16.8627 secs

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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 27, 2003, 15:00:45; search time 12.4655 Seconds (without alignments) 2652.940 Million cell updates/sec

US-10-040-863-11 1850 1 MLVVQMPFSFPMAHFILFVF...........AAFLDFWTGIAADLSPLLKH 344 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224

283224 segs, 96134422 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by charce to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES		QI	A56098	B56392	A56392	A36047	S46494	S51582	T44328	T20745	н87911	T32309	131916	T32294	H71976	T25334	T02798	T21051	T32307	T33253	T20572	T26275	T25390	T22068	T25307	T25309	T15140			T32692	æ
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		Score	00	m	1093.5	õ		593	195	181.5		155	144.5		138		131.5	131	129.5	122	120.5	120	118.5	118	115.5	115.5	114	101	100	93	91
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T34406	H84828	JC5432	532437	E72398	JC5137	S60416	D69252	AH3171	A53595	E97717	AC2861	B97638	A84556	G70978	A72012
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339	401	575	1462	451	460	1489	420	1085	483	805	252	276	396	718	974
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30	31	32	m	34	50	36	37	oc or) Ф) М	40	4.1	42	1.4	44	45

ALIGNMENTS

RESULT 1 A56098 alpha(1,2)fucosyltransferase Sec2, long form - human C;Species: Home sapiens (man) C;Date: 03-0ct-1995 #sequence_revision 03-0ct-1995 #text_change 21-Jul-2000 C;Accession: A56098 R;Kelly, R.J.; Rouquier, S.; Giorgi, D.; Lennon, G.G.; Lowe, J.B.	J. Biol. Chem. 270, 4640-4649, 1995 A;Title: Sequence and expression of a candidate for the human Secretor blood group al A;Reference number: A56098; MUID:95181460; PMID:7876235 A;Reference number: A56098	A;Status: preliminary A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-343 <kel> A;Residues: 1-343 <kel> C;Genetics: C;Genetics: GB:U17894; NID:g687618; PIDN:AAC24453.1; PID:g687619 C;Genetics: A;Genetics: CA:A;Genetics: A;Genetics: A;Gene</kel></kel>	A/CLOSS-Telletences: Sub-licols), OMIM.102100 A.Map position: 19413.3-19913.3 C:Keywords: glycoprotein; Golgi apparatus; transmembrane protein	Query Match Best Local Similarity 99.7%; Pred. No. 5.7e-149; Matches 343; Conservative 0; Mismatches 0; Indels 1; Gaps 1;	1 MLVVQMPFSFPWAHFILEVFTVSTIFHVQRLAKIQAMWELPVQIPVLASTSKALGPSQL 60 	61 RGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQNHSTLAPIFRITLPVLHSATAS 120 	121 RIPWQNYHLNDWMEEDXRHIPPGEXVRFTGYPCSWTFYHHLRQEILQEFTLHDHVREEAQ 180 	181 KFLRGLOVNGSRPGTFVGYHVRRGDYVHVMPKVWKGVVADDRRYLQQALDWFRARYSSLIF 240 	241 VVTSNGMANCRENIDTSHGDVVFAGDGIBGSPAKDFALLTQCNHTİMTIGTFGINAAYLT 300 	301 GGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLIKH 344
RESULT A56098 alpha(1 C; Specio C; Date: C; Acces R; Kelly	J. Biol A,Title tes wit A;Refer A;Acces	A; Statu A; Moleç A; Resid A; Cross C; Genet A; Genet	A; Map p C; Keywo	Query Best Match	QY Db	QY Db	QY 1	QY	QA Dp	Qy

Qy 161 LRQEILQBFTLHDHVREBAQKFLRGLQVNGSRPGTFVGYHVRRGDYVHYWPKVWKCVV 218 11:3:	SULT 4 6047 lactoside 2- Species: Hom Accession: A Larsen, R.D. Co. Natl. Ac	A Accession: A36047 A Status: preliminary A Status: preliminary A Molecule type: MRNA A Residues: 1-365 < LAR> A CLOSS-references: GB:M3551; NID:g183887; PID:g306830 C Keywords: g1ycosyltransferase; hexosyltransferase; transmembrane protein C Keywords: g1ycosyltransferase; hexosyltransferase; transmembrane protein C Keywords: g1ycosyltransferase; hexosyltransferase; transmembrane protein C Matches 209; Conservative 41; Mismatches 79; Indels 21; Gaps 4; Matches 209; Conservative 41; Mismatches 79; Indels 21; Gaps 4; A CO	QY 54 ALGPSQLRGWWTINAIGRLGNQMGEXATLYALAKNNGRPAFIPAQMHSTLAPIFRITLEV 113	QY 292 FGIWAAYLTGODITYLANYTLPDSFFLKIFKPEAAFLPEWTGIAADLSPL 341
beta-galactoside alphal,2-fucosyltransferase II - rabbit C:Species: Cryctolagus cuniculus (domestic rabbit) C:Species: Cryctolagus cuniculus (domestic rabbit) C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 05-Nov-1999 C;Accession: B56392 R;Hitoshi, S.; Kusunoki, S.; Kanazawa, I.; Tsuji, S. R;Hitoshi, S.; Kusunoki, S.; Kanazawa, I.; Tsuji, S. R;Hitoshi, S.; Kusunoki, S.; Manazawa, I.; Tsuji, S. R;Hitoshi, S.; Kusunoki, S.; Mulb:95283880; PMID:7721792 A;Reference number: A56392; MUD:95283880; PMID:7721792 A;Residues: I-354 CHIT> A;Residues: I-354 CHIT> A;Cross-references: GB:X80225; NID:9854356; PIDN:CAA56512.1; PID:9854357 C;Keywords: transmembrane protein	dels 11; Ga dels 11; GaRGMWTINAIGR REGMWTINAMGR REGWWTINAMGR ASRIPWONYHLND	13.2 WMEEEYRHIPPGEYVRFTGYPCSWTFYHERQEI	RESULT 3 A56392 beta-galactoside alphal, 2-fucosyltransferase I - rabbit C;Speciaes: Oryclodagus cuniculus (domestic rabbit) C;Speciaes: Oryclodagus cuniculus (domestic rabbit) C;Speciaes: Oryclodagus cuniculus (domestic rabbit) C;Accession: A56392 R;Hitoshi, S; Ksunnoki, S; Kanazawa, I:; Tsuji, S. R;Hitoshi, S; Ksunnoki, S; Kanazawa, I:; Tsuji, S. A;Title: Molecular cloning and expression of two types of rabbit beta-galactoside alphal A;Reference number: A56392; MUID:95238380; PMID:7721792 A;Status: preliminary A;Molecula type: MRID:A;A;A;A;A;A;A;A;A;A;A;A;A;A;A;A;A;A;A;	A.Crossreferences: GB.X80226; NID:g854354; PIDN:CAA56513.1; PID:g854355 C; Keywords: transmembrane protein Query Match Best Local Similarity 67.0%; Pred. No. 9.6e-86; Matches 203; Conservative 38; Mismatches 59; Indels 3; Gaps 2; QY 41 LPVQIPVLASTSKALGPSQLRGMWTINALGRLGNQMGFYATLYALAKMNGRPAFIPAQMH 100 58 LPVTSPASNASSCAGRPAAPSGIWTHPDGREGNQMGQYATLALAGLAGNGRRAFILPAMH 117

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14;

Gaps

62;

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R; Yamasaki, S.; Shimizu, T.; Hoshino, K.; Ho, S.T.; Shimada, T.; Nair, G.B.; Takeda, Gene 237, 311-332, 1999
A; Title: The genes responsible for O-antigen synthesis of Vibrio cholerae 0139 are classecrece number: 222749; MUID: 99453293; PMID: 10521656
A; Reference number: 222749; MUID: 99453293; PMID: 10521656
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-281 < YAM>
                                                                                                                                                                                                                                                                A; Cross-references: EMBL: AB012957; NID: 94115688; PIDN: BAA33632.1; PID: 93721682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-363 <WILD.
A;Coss-references: EMBL:292830; PIDN:CAB07352.1; GSPDB:GN00023; CESP:Flla5.5
A;Experimental source: clone Flla5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C;Accession: T20745
  C;Date: 21-Jan-2000 *sequence_revision 21-Jan-2000 *text_change 28-Jul-2000 C;Accession: T44328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----STLAPIFRITLPVLHSAT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----SATASRIPWQNYHINDWMEEEYRHI-----PPGEYVRFTGYPCSWTFYHHL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 KGSSNRLSRILRRLGW--LKKNTYYAEKQRTIYDVSVFMQAPRYL--DGYWQNEQYFSQI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 RQEILQEFILHDHVREEAQKFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADR 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222 RYLQQALDWFRARYSSLIFVVTSNGMAWCREN---IDTSHGDVVFAGDGIEGSPAKDFAL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 DYYKRAVDYIKEKIEAPVFFVFSNDVAWCKDNFNFIDSP----VFIED--TQTEIDDLML 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 SSSRLGNHLFELASVLSISRELQRVPTFFIENCYHEKMWEDSNTLIPGLMNHFLIINGSV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 ILFVFTVSTIFHVQQRLAKIQAMWEL-PVQIPVLASTSKALGPSQLRGMWTINAI---- 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --- YPPAQINFRTSRKYISSNYA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 GGLGNQLFQYAVGRAIAIQYGVPLKLDVSAYKNYKLHNGYRLDQFNINADIANEDEIFHL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.8%; Score 181.5; DB 2; Length 363; 23.3%; Pred. No. 8.6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 GRIGNOMGEYATLYALAKMNGRP-----AFIPAOMHSTL-APIFRITLPVLH---
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55/2; 136/3; 175/3; 210/2; 243/1; 299/1; 330/3
                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 10.5%; Score 195; DB 2; Length 28: Best Local Similarity 26.6%; Pred. No. 4.4e-09; Matches 77; Conservative 46; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                        A; Experimental source: strain 022
C; Genetics:
A; Note: wbla
C; Superfamily: Vibrio cholerae hypothetical protein wbla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein F11A5.5 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    279 LTQCNHTIMTIGTFGIWAAYLTGG-DTIYLANYT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Gardner, A. submitted to the EMBL Data Library, March 1997 A;Reference number: 219319 A;Accession: T20745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 LFWMILVYSIF-----LIRAMHEEDPMEVP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: CESP:F11A5.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 5
A; Introns: 42/1;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A) Cross-references: EMBL:L26009; NID:9414814; PIDN:AAB41514.1; PID:9554438
R) Piau, J.P.; Labarriere, N.; Dabouls, G.; Denis, M.G.
Biochem, J. 300, 623-626, 1994
A) Title: Evidence for two distinct alpha-(1,2)-fucosyltransferase genes differentially A) Reference number: S46493; MUID:94280382; PMID:8010942
A) Status: preliminary
A,Title: Evidence for two distinct alpha-(1,2)-fucosyltransferase genes differentially A,Reference number: S46493; MUID:94280382; PMID:8010942
A,Accession: S46494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                galactoside 2-alpha-L-fucosyltransferase (EC 2.4.1.69) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1995 #sequence_revision 17-Nov-1995 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152 PCSWTFYHHLRQEILQEFTLHDHVREEAQKFLRGLQVN--GSRPGTFVGVHVRRGDYVHV 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 MPKVWKGVVADRRYLQQALDWFRARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIE 269
                                                                                                                                      A; Cross-references: EMBL:L26010; NID:g414816; PIDN:AAB41515.1; PID:g414817 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                              213 VWKGVVADRRYLQQALDWFRARYSSLIFVVTSNGMAMCRENIDTSHGDVVFAGDGIEGSP 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273 AKDFALLTQCNHIIMTIGTFGIWAAYLTGGDTIYLANYTLPDSPFLKIFKPBAAFLPEWT 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 AKDFALLTQCNHTIMTIGTFGIWAAYLAGGDTIXLANYTLPDSPELKVFKPEAAFLPEWV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                          Length 159;
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hypothetical protein wblA [imported] - Vibrio cholerae
C;Species: Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C, Accession: S51582; 846493
R; Plau, J.P.; Labarriere, N.; Dabouis, G.; Denis, M.G. submitted to the EMBL Data Library, November 1993
A; Reference number: S51582
A; Accession: S51582
                                                                                                                                                                                                                                                                          Score 623; DB 2; L
Pred. No. 5.3e-46;
6; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.1%; Score 593; DB 2; 74.6%; Pred. No. 1.7e-43; tive 16; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A)Cross-references: EMBL:L26009
C; Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                  A;Gene: FTB
C;Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270 GSPAKDFALLTQCNHTIMTIGT 291
                                                                                                                                                                                                                                                                                33.7%;
88.5%;
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Best Local Similarity 74.69
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                     Best Local Similarity 88.5
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        333 GIAADLSPLLK 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 9-135 <P12>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-142 <PIA>
                                                                                              A; Molecule type: mRNA
A; Residues: 1-159 <PIA>
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Gaps

Db 369 LHFFCPGPREVDMAILKSCDSVIISTGTFGWWSAYLNVNASPDVYYKHWPAPGSVM 425 QY 318 LKIFKPEAAFLPEWTGI 334	RESULT 10 T32309 hypothetical protein F31F4.11 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: 29-oct-1999 #sequence_revision 29-oct-1999 #text_change 20-Jun-2000 C; Accession: T32309 R; Blanchard, M; Kramer, J; Elliott, G; Twyman, B. submitted to the EMBL Data Library, September 1997 A; Description: The sequence of C: elegans cosmid F31F4.	A.Accession: 132309 A.Accession: 132309 A.Molecule type: DNA A.Molecule type: DNA A.Molecule type: DNA A.Molecule type: DNA A.Molecule type: DNA A.Molecule type: DNA A.Molecule type: DNA A.Molecule type: DNA A.Molecule type: DNA A.Molecule type: DNA A.Molecule type: DNA A.Molecule type: DNA A.Molecule type: MBL:AF024503; PIDN:AAB70387.1; GSPDB:GN00023; CESP:F3IF4.11 A.Molecule to the type: Strain Bristol N2; clone F3IF4 A.Gene: CESP:F3IF4.11 A.Molecule type: A.Generian type: SP/2; 179/3; 214/2; 248/1; 283/3; 329/1; 360/3 C.Superfamily: Caenorhabditis elegans hypothetical protein C14C6.3	Query Match Best Local Similarity 20.4%; Pred. No. 1.8e-05; Matches 77; Conservative 47; Mismatches 110; Indels 144; Gaps 18; QY 18 FVFTVSTIFHVQORLARIQAMWELPVQIPVLASTSKALGPSQLRGWATINALGRAGN 74 :	QY 133 MEEEYRHIPPGEXVRFTGYPCSWTEYHHIROEILQEFTLHDHYREEAQKFLRGLQVNGSR 192	SULT 11 1916 1916 Species: Species: Date: 29 Accession Sammons, Descript.
OY 119 ASRIPWONYHLNDWMEBEYRHIPPGEYVRFTGYPCSWFFYHHLRQEILQE 168	227 ALDWFRARYSSLIFVVTSNGMAMCRENIDTSHGDVVFAGDGIE		A; Reference number: A7500; Union Paramator C. Elegans: a platiorm for investigating biology Note: see websites genome. Wuld. 9969696; J. Philo: 9969696; A; Note: see websites genome. Wustl. edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/ biology Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A; Accession: R87911 A; Note: preliminary A; Molecule type: DNA A; Residues: 1-443 <sto> A; Cross-references: GB:chr_I; PIDN: AAC16988 1; PID: 93150470; GSPDB: GN00019; CESP: B0205.4 C; Genetics: contains weak similarity to fucosyltransferases C; Genetics: A; Map position: 1 A; Map position: 1</sto>	Query Match Best Local Similarity 20.48; Score 176; DB 2; Length 443; Matches 89; Conservative 63; Mismatches 145; Indels 140; Gaps 17; QY 15 FILEVETVSTIPHVQRLAKI-QAMWELPVQIPVLA 49 29 YILFLENISKTRILTPEERPATYMKRNVFYQSGNEAILNOCPWPISVENVINRYSVLE 86 QY 50 STSKALGPSQLRGMWIINAIGHGONGEYATLYALAKANGRPAFIDAQMHSTLA 104 B97 NSGKRYIFSDFGYSQ	OY 146 VRFTGYPCSWTFYHHLROEILOB-FTLHDHVRE

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hypothetical protein T26H5.8 - Caenorhabditis elegans
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C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: 29-oct-1999 #sequence_revision 29-oct-1999 #text_change 20-Jun-2000
C.Accession: T32294
R.David, M.; Wohldmann, P.; Bauer, C.; Clarke, K.
Submitted to the EMBL Data Library, September 1997
A.Description: The sequence of C. elegans cosmid K06H6.
A.Accession: T32394
A.Accession: T32394
A.Accession: T32394
A.Accession: T32394
A.Accession: T32594
A.Accession: T325 AAV>
A.Accession: T335 ABV>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: DNA
A;Residues: 1-348 <SAM>
A;Cross-references: EMBL:AF016654; PIDN:AAB66030.1; GSPDB:GN00020; CESP:C17A2.4
A;Experimental source: strain Bristol N2; clone C17A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 5
A;Introns: 17/1; 32/2; 58/1; 111/3; 150/3; 184/2; 218/1; 243/3; 272/1; 303/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C14C6.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 MFELAAVLGISRMLNRTATFFIEDEIYRRMIESSKEAIPGLVGQFEILNGKVPLYIKNTK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 MGEYATLYALAKMNGRPA--FIPAQMHSTLAPIFRITLPVL---HSATASRIPW--QNYH 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----DWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHDHVR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 --DFLDDSSQDF-----GRIPRSNQRTHVICVHARRGDFVDV-----GFQAADPDFI 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQALDWFRARYSSLI------FVVTSNGMAWCR---EN--IDTSHGDVVFAGDGI--E 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 VLLVLTLVIV------VQLYKSATAEIPPLRQESFLIMKKRLSSRMAPTA--RLGNH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171 LHDHVREEAQKFLRGLQVNGSRPGT----FVGVHVRRGDYVHVMPKVWKGV-VADRRYL 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 129; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 RLGNQMGEYATLYALA-KMNGRPAF-IPAQMHSTLAPIFRITLP------VLHSATASR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 ILFVFTVSTIFHVQQRLAKIQAMWELPVQIPVLASTSKALGPSQLRGMWTINAIGRLGNQ 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 I---PWQ-----NYHLNDWMEEEYRHIPPGEXVRFTG-YPCSWTFYHHLRQEILQEFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 2
A;Introns: 94/3; 133/3; 168/2; 272/1
C;Superfamily: Caenorhabditis elegans hypothetical protein C14C6.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 22.1%; Pred. No. 0.00012;
Matches 62; Conservative 61; Mismatches 86; Indels 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.6%; Score 141.5; DB 2; Best Local Similarity 20.4%; Pred. No. 0.0002; Matches 77; Conservative 53; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSPAKDFALLTQ-CNHTIMTI--GTFGIWAAYLTGGDTIY 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: CESP:K06H6.6
                                                                                                                                                                                                                                                                                                                     A;Gene: CESP:C17A2.4
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QQ	Db 121 INTRCCVFVDPLIHEHNNDEYLHL-DGRFYQAWKYFPSMRNEL	NEL1163
Qy	177 EEAQKFLRGLQVNGSRP	VADRRYLQQALDWF 231
QO	Db 164GYLKTSENFGSLFKSNETSFVTCVHIRRGDFKRVGFAESDEWF	:: :!! GFAESDEWF 206
δ	232 RARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIE 1	
an	ZO! TRNAREV	
Q <u>y</u>	QY 271 SPAKDFALL-TQCNHTIMTIGTFGIWAAYLIGGDTIYLANYTLPDSFFKKI	DSPFLKI 320 :: YMDIRETRDNV 302
οy	321	
Db	303 YRNGGLNPYDYYL	
RESU	RESULT 13	
H/IS prob C;Sp	elicobacter	pylori (strain J99)
A;Vā C;Da	A;Variety: strain J99 C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_	_change 28-Jul-2000
C;AC R;Al	C;Accession: H71976 R;Alm, Fa.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, F;Alm, Fa.; Ling, L.S.L.; Moir, D.; Mills, S.D.; Jiang, Q	1, E.D.; Doig, P.C.; Smith, D.
Natu A, Ti	wo unrelated i	ates of the
A; K A; BC A; St		
A; MC A; Re A; C;	A; Molecule type: DNA A; Residues: 1-299 <arn> A; Cross references: GB: AE001447; GB: AE001439; NID: 941545</arn>	583; PIDN:AAD05659.1; PID:9415
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C; St	al protein wbl	K
ÕĂĬ	Query Match 7.5%; Score 138; DB 2; Ler Best Local Similarity 22.3%; Pred. No. 0.00035; Matches 67; Conservative 45; Mismatches 137; J	Length 299; Indels 52; Gaps 11;
QY	66 INAIGRLGNOMGEYATLYALAKMNGRPAFI	CHSATAS :
qq	6 VQICGGLGNQMFQYAFAKSLQKHSNTPVLLD	LFPIDLPYASAK 62
Qy	121 RIP-WQNYHLNDWM	16
Q	63	YFYGYF'QDPRXE'DA1 122
Oy	OY 162 ROEILQEFILHDHVREEAQRFIRGLQ-VNGSRPGTFVGVHVRRGDYVHVMPKVWK	
qq	123	IRRGDYVGI 174
ÓΫ	216	VVFAGDGIEGSPAKD 275
qa	Db 175 GCQLGIDYQKKAVEYMAKRVPNMELFVFCEDLKF-TQNLDLGYPFMDMTTRDKDEEAYWD	MOMTTRDKDEEAYWD 233
ΟY	276 FALLTQCNHTIMTIGTFGIWAAYLTGGDTIXLANYTLP	KIFKPEAAFLPEWTG 333
Dp	234 MLLMQSCKHGIIANSTYSWWAAYLINNPGKIII	-GPKHWLFGHENILCKEWVK 285
QY	QY 334 I 334	
qq	Db 286 I 286	
RES	RESULT 14	er)
1	10001	

us-10-040-863-11.rpr

aenorhabditis elegans ct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000 T25334; T26600 the EMBL Data Library, November 1996	यस	
A) Accession: T25334 A) Status: preliminary; translated from GB/EMBL/DDBJ A) Molecule type: DNA A) Molecule type: DNA A) Residues: 1.392 <wil> A) Cross-references: EMBL:282056; PIDN:CAB04857.1; GSPDB:GN00023; CESP:T26H5.8 A) Experimental source: clone T26H5 B) Wall, Wall ted to the EMBL Data Library, October 1998 A) Reference number: Z20243 A) Accession: T26600 A) Status: preliminary; translated from GB/EMBL/DDBJ A) Molecule type: DNA A) Residues: 1-392 <wiz></wiz></wil>		### ### ##############################
A;Cross-references: EMBL:AL032620; PIDN:CAA21488.1; CESP:T26H5.8 A;Experimental source: clone Y36E3A C;Genetics: A;Genetics: A		167 QEFTLHDHVI :: :: :: 179 EQLDVVEYYC 207 VHVMPKVWKC 225LLPLHLLV 263 FAGDGIBGSE 264 MPRDVLE 323 PEAAFLPE
SRIPWQNYHLNDWMEEBYRH-IPPGGEVVRTGYPCSWTFYHHLRQEILQEFTLH 172	S S O D	
RESULT 15 T02798 hypothetical protein L549.10 [imported] - Leishmania major (strain Friedlin) C;Species: Leishmania major C;Species: Leishmania major C;Species: Leishmania major C;Species: Leishmania major C;Species: Leishmania major C;Species: Leishmania major C;Species: Leishmania major Fxidle: Leishmania major Fxidle: Leishmania major Fxidlin chromosome I has an unusual distribution of protein-c A; Accession: B81456 A;Status: Preliminary A; Moll: Species: Muld:		

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11;
                                                                                                                                     -- QMHSTLAPIFRITLPVL-----HS 116
                                                                                                                                                            -WQN-----YHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEIL 166
                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                 :: | || :
DAAVRQLLGGLLLQSPSLLRQQQSPVDSAQAPTAGAPP------225
                                                                                                                                                                                                                                                                                                                                            SVVADRRYLQQALDWFRARYSSLIFV----VTSNGMAWCRENIDTSHGDVV 262
                                                                                                                                                                                                                                                                                                                                                                 : |: : : : || :| : |
VFCDEERFGRTVVGYFRTKYKGAVMVSLVCAATEASAISARPTASSPSVPI 283
                                                                 MWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPA-------97
                                                                                        | | :| :||:
RITTNIVGGMGNQLELVANLLATAHRIGIPAYLEAVPFSSSAEDPRPTYWD 72
7.1%; Score 131.5; DB 2; Length 349; crity 18.1%; Pred. No. 0.0015; onservative 48; Mismatches 125; Indels 131;
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

May 27, 2003, 14:53:11; Search time 10.0683 Seconds (without alignments) 1417.108 Million cell updates/sec Run on:

US-10-040-863-11 1850 1 MLVVQMPFSFPMAHFILFVF......AAFLPEWTGIAADLSPLLKH 344 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched: 112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SwissProt_40:* Database :

SUMMARIES

Description	0981 h g 0982 sus 8113 bos	oryc	ratt	mus mus	P19526 homo sapien 029643 sus scrofa		caenorhab	P79282 s alpha-(1,	n alpha-(E	P53115 saccharomyc	00-10 rana careso	raisto	P968/5 mycobacteri	cavia porc		escherichi	neisseria	escheri	Д	schizos		rhizobiu	arabido	wns wns	rattus nor	nomo s	salmonel
ID	2,5,5	1 1 '	FUT1_RAT	1 1	FUT1_HUMAN	1 1		FUTE_PIG	FUT8_HUMAN	FUTB_MOUSE	YGPO_YEAST	ALN_KANCA	MIAA_RALSO	- 1	S6A4_CAVPO	CBPA_ANOGA	æ		- 1	FUT8_BOVIN	S	LPH_RAT	NOEA_RHIME	UT6_ARAT	S6A4_MOUSE	S6A4_RAT		BCSA_SALTY
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	346	354 368	376	376	365	159	365	575	575	ξ,	1489	484	323	718	630	433	660	328	1048	575	1211	9	476	537	630	630	1279	874
% Query Match Length	021	. 0		, œ	ω α	. n	æ				•	•	4.6	4.6	4.6	4.5	4.5	4.5	4.5	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4 . 4
Score	528	າທອ	100	083	080	av e	155	92	06	06		86.5	8 2		84.5	84	83.5	83	82.5	82	82	82				81.5		
	1 7 7 8	J 44 R.	100	~ 80	ω. C) H	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

Q92448 pichia past	Q56855 yersinia en	095897 homo sapien	Q9xqv2 heterocapsa	P87078 candida alb	P40601 photorhabdu	P28820 bacillus su	Q01365 barley yell	006458 thermus the	P56786 arabidopsis	Pl3887 ross river	Q47266 erwinia chr
K6P1_PICPA	FES_YEREN	NOE2_HUMAN	PSAB_HETTR	TOP2_CANAL	LIP1_PHOLU	PABB_BACSU	POL2_BAYMG	TRES_THETH	YCF2_ARATH	POLN_RRVN	HMPA_ERWCH
Н	Н	П	Н		-	٦	Н	1	Н	Н	г
056	353	454	776	1461	645	470	890	963	2294	2479	395
4.3	4.3	4.3	4.3	4.3	4.2	4.2	4	4.2	4.2	4.2	4.2
80	79.5	79	79	79	78.5	7.8	78	7.8	7.00	78	77.5
34	35	36	37	. cc	0	4	4	4.2	4 4	4	45

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHORT ISOPORM.

FOR SHORT ISOPORM.

CYTOPLASMIC (POTENTIAL).

SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).

LUMENAL, CATALYTIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

Y-Y (IN XHOSA POPULATION).

/FILG=VAR_003422.

/FILG=VAR_003423.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 KFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATAS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 RIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWIFYHHLRQEILQEFTLHDHVREBAQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VVISNGMANCRENIDISHGDVVFAQDGIEGSPAKDFALLTQCNHTIMIIGTFGINAAYLT 300
                                         ALTERNATIVE PRODUCTS:

ALTERNATIVE PRODUCTS:
TWO FORMS ARE PRODUCED BY THE USE OF
ALTERNATIVE INTIATION CODONS IN THE SAME READING FRAME.

TISSUE SPECIFICITY: SMALL INTESTINE, COLON AND LUNG.

MISCELLANBOUS: THERE ARE TWO GENES (FUTI AND FUT2) WHICH ENCODE
GALACYOSIDE 2.1-FUCGSYLTRANSFERASE. THEY ARE EXPRESSED IN A
TISSUE-SPECIFIC MANNER WITH EXPRESSION RESTRICTED TO CELLS OF
MESODERMAL OR ENDODERMAL ORIGIN RESPECTIVELY.

SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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PATHWAY: Glycosylation.
SUBCELDLAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymorphism.
13 GALACTOSIDE 2-L-FUCOSYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GALACTOSIDE 2-L-FUCOSYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                              InterPro: IPR002516; GT_11.
Pfan: PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal-anchor; Golgi stack; Alternative initiation;
Blood group antigen; Polymorphism:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tch 99.1%; Score 1832.5; DB 1; Length 343; al Similarity 99.7%; Pred. No. 9.2e-150; 343; Conservative 0; Mismatches 0; Indels 1;
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D -> N (IN XHOSA POPULATION)
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12066D9CF175E13A CRC64;
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TRANSMEM
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CARBOHYD
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                                                                                                                                                      010982; 029044; 019100;
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 2 (EC 2.4.1.69) (GDP-L-fucose:beta-
D-galactoside 2-alpha-L-fucosyltransferase 2) (Alpha(1,2)Fr 2)
240 VVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                  MEDINE-97468270; PubMed-9321466;
Meijerink E., Fries R., Voegeli P., Masabanda J., Wigger G.,
Stricker C., Neuenschwander S., Bertschinger H.U., Stranzinger G.;
"Two alpha(1,2) tucosyltransferase genes on porcine chromosome 6q11
are closely linked to the blood group inhibitor (S) and Escherichia
coli F18 receptor (ECF18R) loci.";
Mamm. Genome 8:736-741(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metázoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cohney S., Mountouris E., McKenzie I.F.C., Sandrin M.S.;
"Molecular cloning and characterization of the pig secretor type
alpha(1,2)fucosyltransferase.";
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Golgi stack; Signal-anchor.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                              3C1 GGDIIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 69-80; 119-133 AND 316-334
                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 69-334 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U70881; AAB81883.1; ~.
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                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                           (Fucosyltransferase 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X99621; CAA67932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                       Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9823;
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                                                                                                                                      5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUT2_BOVIN STANDARD; PRT; 344 AA.
028113,
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUV-2002 (Rel. 41, Last annotation update)
6alactoside 2-L-fucosyltransferase 2 (EC 2.4.1.69) (GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase 2) (Alpha(1,2)FT 2)
                                                                                                                                                                                                                                                                             181 KFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIF 240
                                                                                                                                                                                                                                                                                                                              237 VVSSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNHTVMTIGTFGIWAAYLA 296
                                                                                                                                                                                                              61 RGMWTINAIGRLGNQMGEXATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATAS 120
                                                                                                                                                                                                                           SR KGMWTINAIGRIGNOMGEXATLYALARMNGRPAFIPPEMHSTLAPIERITLPVLHASTAR 117
                                                                                                                                      Gaps
                                                                                                                                                            1 MLVVQMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAMWELPVQIPVLASTSKALGPSQL 60
                                                                                                                                                                                     57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP + alpha-i-fucosyl-1,2-beta-D-galactosyl-R.
PATHWAY: Glycosylation:
SUBCELLULAR LOCATION: TYPE II MENBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                  241 VVTSNGMAWCRENIDISHGDVVFAGDGIEGSPAKDFALLIQCNHTIMTIGTFGIWAAYLT
                                                                                                                                                                                121 RIPWONYHLNDWMEEEYRHIPPGEYVRFIGYPCSWTFYHHLRQEILQEFTLHDHVREEAQ
         LUMENAL, CÁTALYTIC (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).

R-LINKED (GLCNAC. . ) (POTENTIAL).

R-LINKED (GLCNAC. . )
                                                                                                                                      .,
                                                                                                             Length 340;
                                                                                                                                      Indels
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                                                                         -> H (IN REF. 3).
0629F1C04FC206AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                               GGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 344
                                                                                                                                      34;
                                                                                                             Score 1528; DB 1;
Pred. No. 1.1e-123;
                                                                                                                                      24; Mismatches
   (POTENTIAL)
                                                                                       38987 MW;
                                                                                                               82.6%;
82.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X99620; CAA67931.1; -
                                                                                                                                         Matches 282; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Fucosyltransferase 2).
                                                              305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
             29
185
251
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340 AA;
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                                                                                                                            Similarity
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Submitted (
               DOMAIN
CARBOHYD
CARBOHYD
                                                              CARBOHYD
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Best Local S
                                                                                       SEQUENCE
                                                    CARBOHYD
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240 FVVTSNGMAWCRENIDISHGDVVFAGDGIEGSPAKDFALLIQCNHTIMTIGTFGIWAAYL 299
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"Molecular cloning and expression of two types of rabbit beta-
galactoside alpha 1,2-fucosyltransferase.";
J. Biol. Chem. 270:8844-8850(1995).

J. Biol. Chem. 270:8844-8850(1995).

(1,2)GALBETA-) CALLED THE H ANTIGEN WHICH IS AN ESSENTIAL
SUBSTRATE FOR THE FINAL STEP IN THE SOUGHLE AND B ANTIGEN
SYNTHESIS PATHWAY. H AND SE BIXTHES FUCOSYLATE THE SAME ACCEPTOR
SUBSTRATES BUT EXHIBIT DIFFERENT KM YALUES.

-!- CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 LRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATA 119
                                                                                                                                                                                                     SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MLVVQMPFSFPNAHFILFVFTVSTIFHVQQRLAKIQAMWELPVQIPVLASTSKALGP-SQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotation update)
17-JUN-2002 (Rel. 41, Last annotation update)
18-JUN-2002 (Rel. 41, Letoosyltransferase)
18-JUN-2003 (BDP-L-10008e:beta-D-10008)
18-JUN-2003 (BDP-L-10008e:beta-D-10008)
18-JUN-2003 (BDP-10008)
18-JUN-2003 (BD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | MFSTQTFFFFPTAPFILFVFTASTIFHLHQRLEKMQPTWELEALEPATMETPSRPQPRPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 SRIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHDHVREEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 OKFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                               (LUMBNAL, CATALYTIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
        InterPro; IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Transferase, Glycosyltransf_11; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lagomorpha; Leporidae; Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (PC
F35AC33F1B7B9F68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 AGGETIYLANYTLPDSPFLKIFKPEAAFLPKWIGIPADLSPLKH 344
                                                                                                                                                                      CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 4.1e-122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1510;
                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95238380; PubMed=7721792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39320 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81.6%;
82.3%;
                                                                                                                          Golgi stack; Signal-anchor.
DOMAIN 1 7
IPR002516; GT_11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUT2 OR SEC1 OR RFT-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Fucosyltransferase 2)
                                                                                                                                                                                                              28
                                                                                                                                                                                                                                                                                                 344
189
255
283
309
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                                                                                                                                                                                                                                                                                             29
189
255
283
309
344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUT2_RABIT
Q10983;
                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bhoinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MNY-2000 (Rel. 39, Created)
30-MNY-2000 (Rel. 39, Last sequence update)
15-UNY-2002 (Rel. 41, Last annotation update)
63-actoside 2-fucosyltransferase 2 (EC 2.4.1.69) (GDP-L-fucose:beta-
D-galactoside 2-alpha-L-fucosyltransferase 2) (Alpha(1,2)FT 2)
(Fucosyltransferase 2) (FUT-III).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 WMEEEYRHIPPGEYVRFIGYPCSWTFYHHLRQEILQEFTLHDHVREEAQKFLRGLQVNGS 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 LGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATASRIPWQNYHLND 131
                                                                                                                                                                                                                                                                                                                                      SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                   -!- TISSUE SPECIFICITY: SALIVARY AND LACTATING MAMMARY GLANDS.
-!- TISSUE SPECIFICITY: SALIVARY AND LACTATING MAMMARY GLANDS.
-!- MISCELLANEGUS: THERE ARE THREE GENES (FUT1, FUT2 AND FUT3) WHICH ENCODE GALACTOSIDE 2-LE-FUCOSYLLENANFERASE IN RABBIT. THRY ARE EXPRESSED IN A TISSUE-SPECIFIC, MANNER.
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 HFILEVFTVSTIFHVQQRLAKIQAMWELPVQIPVLASTSKALGPSQL--RGMWTINAIGR 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 YFLFTIFVVSTVFHCHQRLALVPAPWAYSARVVVV-----PGHLPREGMWTINAMGR 80
              PATHWAY: Glycosylation.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.
TISSUE SPECIFICITY: SALLVARY AND LACTATING MAMMARY GLANDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 RPSTFVGVHVRRGDYVRVMPQVWKGVVADRGYLEQALDWFRAPTAPPVFVVTSNGMAWCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLTGGDTIYLANYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192 RPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIFVVTSNGMAWCR
                                                                                                                                                                                                                                                                                                                                                               LUMENAL, CATALYTIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

1 IEZB831F9DA6CC84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41; Indels 11;
                                                                                                                                                                                                                                                EMBL, X80225; CAA56512.1; -.
InterPro; IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 354;
                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 1375.5; DB 1; Pred. No. 1.4e-110; 26; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA.
 alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               312 LPDSPFLKIFKPEAAFLPEWTGIAADLSPLL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           320 APDSPFHLVFKPEAAFLPEWVGITANMGRAL 350
                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                          40035 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     74.48;
76.48;
                                                                                                                                                                                                                                                                                                             Golgi stack.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 76.4:
Matches 253; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUT2 OR SEC1.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                  44
197
291
317
354 AA;
                                                                                                                                                                                                                                                                                                             Signal-anchor;
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUT2_MOUSE
P97353;
                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match
                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUT2_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular cloning and expression of a GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase in murine gastrointestinal tract."; submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
-!-CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP + alpha-L-fucosyl-1.2 beta-D-galactosyl-R.
-!-PATHWAY: Glycosylation.
-!-SUBCELLOLAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI (BY SIMILARITY).
-!-SUBCELLOLAR COCTITON: THOSE IN MEMBRANE FROUDE GALACTOSIDE 2-L-FUCOSYLITRANSFERASE.
-!-SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246 GMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLIQCNHTIMTIGTFGIWAAYLTGGDTI 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INAIGRIGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATASRIPWQ 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL). SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 PMAHFILF--VFTVSTIFHVQQRLAKIQAMWELPVQIPVLASTSKALGPSQ----LRGMWT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hitoshi S., Kusunoki S., Kanazawa I., Tsuji S.;
Molecular cloning and expression of a mouse GDP-L-Fucose: beta-D-
galactoside 2-alpha-L-Fucosyltransferase.";
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 PLSTFYLFFVIFVVSTIFHCHRRLGLVPAPW-----ASPSLVVFPPRHMPREGMFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 NYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHDHVREEAQKFLRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIFVVTSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata: Craniata; Vertebrata; Euteleostomi;
Mammalia: Butheria; Rodentia: Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POIENTAL).
LUMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Y09882; CAA71008.1; -.
EMBL; AF115532; AAD25351.1; -.
MGD; M031:109374; Fut2.
Interpro; IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70.2%; Score 1299.5; DB 1; Length 368; 73.6%; Pred. No. 4.8e-104;
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-INTERTIONAL tract; STRAIN-INTERNATION TISSUE-Gastrointestinal tract; Lin B., Hayashi Y., Saito M., Sakakihara Y., Yanagisawa M., Iwamori M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (Po
4093E853EB37303B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43;
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Best Local Similarity 73.6%; Pred. No. 4.8e-
Matches 245; Conservative 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41464 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Golgi stack.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     368
195
289
315
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195
289
315
368 AA;
                                                                                                                                                         SEQUENCE FROM N.A.
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CARBOHYD
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SEQUENCE
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Best Local Similarity
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Q10979;
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                   Matches
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                                                                                                                                                                                01-001-1996 (Rel. 34, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 1 (EC 2.4.1.69) (GDP-L-fucose:beta-
D-galactoside 2-ralpha-L-fucosyltransferase 1) (Alpha(1,2)FT 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 252 DMAWCRKSITASRGDVAFAGNGLQGSPAKDIALLMQCNHTVITLGTFGIWAAYLTGGDTV 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN, MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI (BY SIMILARITY).
MISCELLANBOUS: THERE ARE TWO GENES (FUTI AND FOT2) WHICH ENCODE GALACTOSIDE 2-L-FUCOSYLTRANSFERASE. THEY ARE EXPRESSED IN A TISSUE-SPECIFIC MANNER WITH EXPRESSION RESTRICTED TO CELLS OF MESODERMAL OR ENDODERMAL ORIGIN RESPECTIVELY.
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Piau J.-P., Labarriere N., Dabouis G., Denis M.G.;
"Evidence for two distinct alpha(1,2)-fucosyltransferase genes
differentially expressed throughout the rat colon.";
Biochem. J. 300:623-626(1994).
-!- CATALYPIC ACTIVITY: GDP-L-fucose + beta-D-galactcsyl-R = GDP
alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LUMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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InterPro; IPRO02216; G7-11.
Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Two distinct rat GDP-L-fucose:b-D-galactoside 2-alpha-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                               fucosyltransferase genes.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C350C737C758B7F8 CRC64;
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                                                                                                                                                         376 AA
                                        306 YLANYTLPDSPFLKIFKPEAAFLPEWTGIAADL 338
                                                            312 YLANFTQPNSPFHTVFKPEAAYLPEWVGIAADL 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Soejima M., Wang B., Koda Y., Kimura H.;
                                                                                                                                                         PRT;
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                                                                                                                                                             STANDARD;
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Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                (Fucosyltransferase 1).
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302
328
376 AA;
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                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
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DOMAIN
                                                                                                                                                             FUT1_RAT
Q10980;
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                                                                                                                             RESULT
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Length 376;

DB 1;

Score 1100.5;

59.5%;

Query Match

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ils-sib.ch).
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01-oCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactoside 2-Ficosyltransferase 1 (EC 2.4.1.69) (GDP-L-fucose:beta-
D-galactoside 2-alpha-L-fucosyltransferase 1) (Alpha(1,2)FT 1)
(Fucosyltransferase 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VWKGVVADRRYLQQALDWFRARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSP 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AKDFALLTQCNHTIMTIGTFGIWAAYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWT 332
                                                                                                                                                                                                                55 AMVCLP--YPSNASSGSPSCPEQSLLSGTWTITPGGRFGNQMGQYATLLALAQLNGRRAF 112
                                                                                                                                                                                                                                                                                    IPAQMHSTLAPIFRITLPVLHSATASRIPWQNYHLNDWMEBEYRHIPPGEYVRFTGYPCS 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WTFYHHLRQEILQEFTLHDHVREBAQKFLRGLQVN--GSRPGTFVGVHVRRGDYVHVMPK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 292 GKDFALLTQCNHTIMTIGTFGFWAAXLAGGDTVXLANFTLPDSBFLKIFRFKAAFLPEWV 351
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FORM IN TRANS.

-1. TISSUE SPECIFICITY: BRAIN.

-1. MISCELLANEOUS: THERE ARE TWO GENES (FUT1 AND FUT2) WHICH ENCODE

-1. MISCELLANEOUS: THERE TWO GENES (FUT1 AND FUT2) WHICH ENCODE

-1. MISCELLANEOUS: THERE TWO GENES (FUT1 AND FUT2) WHICH ENCODE

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-1. MISCELLANEOUS: THERE ARE TWO GENES (FUT1 AND FUT2) WHICH ENCODE

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-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI.
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-!- SIMILARITY: BELONGS TO THE GLYCOSYLIRANSFERASE FAMILY 11.
                                                                                                                                    37 AMWELPVQIPVLASTSKALGPSQ--LRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95288380; PubMed=7721792;
Hitoshi S., Kusunoki S., Kanazawa I., Tsuji S.;
Hitoshi S., Rusunoki S., Kanazawa I., Tsuji S.;
"Molecular cloning and expression of two types of rabbit beta-
galactoside alpha 1,2-fucosyltransferase.";
J. Biol. Chem. 270:884-8850(1995).
-i-.CHTALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP
alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
                                                            7;
                                                            Indels
                        Pred. No. 5.7e-87;
; Mismatches 59;
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67.0%; Pic.
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                                                                    Conservative
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FUT1_HUMAN
P19526;
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15-DEC-1998 (Rel. 37, Last sequence update)
15-UNA-2002 (Rel. 41, Last annotation update)
Galactoside 2-L-fucosyltransferase 1 (EC 2.4.1.69) (GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase 1) (Alpha(1,2)FT 1)
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TISSUE SPECIFICITY: IN THE ADULT, HIGHLY EXPRESSED IN PANCREAS, TESTES AND EPIDIDYMIS AND TO A LESSER EXTENT IN THYMUS, LUNG, STOMACH, SMALL INTESTINE, COLON, SPLEEN AND UTERUS. NOT EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 STLAPIFRITLPVLHSATASRIPWQNYHLNDWMEEEYRHIPPGEYVRFIGYPCSWTFYHH 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRQEILQEFTLHDHVREEAQKFLRGLQV--NGSRPGTFVGVHVRRGDYVHVMPKVWKGVV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                279 LIQCHHILMTIGTFGIWAAYLIGGDTIYLANYTLPDSPFIKIFKPEAAFLPEWTGIAADL 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 LPVQIPVLASTSKALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMH 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 LPVTSPASNASSCAGRPAAPSGIWTIHPDGRFGNQMGQYATLLALAQLNGRRAFILPAMH 117
                                                                                                          CYTOPLASMIC (POTENTIAL). SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 ADRRYLQQALDWFRARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domino S.E., Hiraiwa N., Lowe J.B.;

Domino S.E., Hiraiwa N., Lowe J.B.;

Molecular cloning, chromosomal assignment and tissue-specific
expression of a murine alpha(1,2)fucosyltransferase expressed in
thymic and epidofymal epithalial cells.;

Biochem. J. 327.105-115(1997).

-!- CATALYTIC ACTIVITY: GDP-L-fucose + beta-D-galactosyl-R = GDP
alpha-L-fucosyl-1,2-beta-D-galactosyl-R.
                                                                                                                                                                                           (UMENNL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
OA47A1786231525C CRC64;
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pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
Signal-anchor; Golgi stack.
DOMAIN
1 12. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                   59.1%; Score 1093.5; DB 67.0%; Pred. No. 2.2e-86;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 2.2e
38; Mismatches
                                                                                                                                                                        (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                            42098 MW;
                                                                          Golgî stack.
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3 29
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nes 203; Conservative
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301
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66
301
327
373 AA;
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STRAIN=NIH Swiss;
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009160;
                                                                                                                                                                                                     DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                               CARBOHYD
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL-ANCHOK (TYPE-II MEMBRANE PROTEIN).
LUMEDAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
63-actoside 2-L-fucosyltransferase 1 (EC 2.4.1.69) (GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase 1)
(Fucosyltransferase 1) (Alpha(1,2)FT 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 AYLQQAMDWFRARHKDPIFVVTSNGMKWCLENIDTSHGDVVFAGNGQEGTPGKDFALLTQ 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46 PVLASTSKALGPSQ----LRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHST 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 LAPIFRITLPVLHSATASRIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCŚWIFYHHLR 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RYLQQALDWFRARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQ 281
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MEDLINE-90370848; Pubmed=2118655;
Larsen R.D., Ernst L.K., Nair R.P., Lowe J.B.; ...
"Molecular cloning, sequence, and expression of a human GDP-L-fucose:beta-D-galactoside 2-alpha-L-fucosyltransferase cDNA that can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
IN BRAIN, HEART, SKELETAL MUSCLE, KIDNEY, LIVER AND BONE MARROW-!- MISCELLANEOUS: THERE ARE TWO GENES (FUT1 AND FUT2) WHICH ENCODE GALACTOSIDE 2-L-FUCOSYLTRANSFERASE.
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11.
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:109375; Futl.
InterPro; IPR002516; GT.11.
Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycoyltransferase; Glycoprotein; Transmembrane; Signal-anchor; Golgi stack.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.6%; Score 1083.5; DB 1; Length 376; 67.0%; Pred. No. 1.6e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21F1D24CFE204106 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 N-
302 N-
328 N-
42255 MW;
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Best Local Similarity 67.0%
Matches 201; Conservative
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Mammalia; Eutheria;
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27
67
302
328
376 AA;
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MISCELLANEOUS: THERE ARE TWO GENES (FUT1 AND FUT2) WHICH ENCODE GALACYOSIDE 2-L-FUCOSYLITANSFERASE. THEY ARE EXPRESSED IN A TISSUE-SPECIFIC MANNEY BEXPRICTED TO CELLS OF MESODERAL OR ENDODERAL ORIGIN RESPECTIVELY.

SIMILARITY: BELONGS TO THE GLYCOSYLITRANSFERASE FAMILY 11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATHWAY: Glycosylation.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
FORM IN TRANS CISTERNAE OF GOLGI.
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-94286534; PubMed-7912436;
Kelly R.J., Ernst L.K., Larsen R.D., Bryant J.G., Robinson J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecular basis for H blood group deficiency in Bombay (Oh) and
                                                                                                                                                                                         Wagner F.F., Flegel W.A.; "Population frequency of "Polymorphism of the hallele and the population frequency of sporadic nonfunctional alleles."; Transfusion 37:284-290(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L -> H (IN PARA-BOMBAY).
/FIId=VAR_009708.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /FTId=VAR_003418.
L -> R (IN BOMBAY H-).
/FTId=VAR_009709.
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        form the H blood group antigen.";
Proc. Natl. Acad. Sci. U.S.A. 87:6674-6678(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            para-Bombay individuals.";
Proc. Natl. Acad. Sci. U.S.A. 91:5843-5847(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                   SEQUENCE FROM N.A., AND VARIANT ALLELES MEDLINE-97240210; Pubmed-9122901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VAŘIANT ARG-242.
MEDLINE=97445117; Pubmed=9299444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M35531; AAA52639.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171
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                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT HIS-164.
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                                                                                                                                                                                                                                                                                                                       11 LAFLLVCVLSVIFFLHIHQDSFPHGLGLSILCPDRRLVTPPVAIFCLPGTAMGPNASSSC 70
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                           ---LAKIQAMWELPVQIPVL-----ASTSK 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97468270; PubMed=9321466; Meiblerink E., Fries R., Voegeli P., Masabanda J., Wigger G., Meibreink C., Ruenschwander S., Bertschinger H.U., Stranzinger G.; Two alpha(1,2) fucosyltransferase genes on porcine chromosome 6q11 are closely linked to the blood group inhibitor (S) and Escherichia are clisely linked ECETBA P. Coli E18 receptor (ECETBA loci."; Mamm. Genome 8:736-741(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 LHSATASRIPWQNYALNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 LAPEVDSRIPWRELQLHDWMSEEYADL-RDPFLKLSGFPCSWTFFHHLREQIRREFTLHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Small intestine;
Meijerink E., Neuenschwander S., Fries R., Dinter A.,
Bertschinger H.U., Stranzinger G., Voegeli P.;
"Expression and activity of porcine alpha(1,2)fucosyltransferases
                                                                                                                                                                                                                                                                                                                                                                           54 ALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HVREEAQKFLRGLQV--NGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartlodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                         21;
                                                                                                                                                                           DB 1; Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
6Galactoside 2-L-fucosyltransferase 1 (EC 2.4.1.69) (GDP-L-fu
D-galactoside 2-alpha-L-fucosyltransferase 1) (Alpha(1,2)FT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FGIWAAYLTGGDTIYLANYILPDSPFLKIFKPEAAFLPEWTGIAADLSPL 341
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                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4F4442EC375C9D9E CRC64;
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/FTIG=VAR_003419.
A -> V (IN BOMBAX H-).
FTIG=VAR_003420.
W -> C (IN BOMBAY H-).
/FTIG=VAR_003421.
                                                                                                                                                                                                                            79;
                                                                                                                                                                           Score 1080.5; DB Pred. No. 2.8e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         365 AA
                                                                                                                                                                                                                               41; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96217559; PubMed=8613146;
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                                                                                                                               41251 MW;
                                                                                                                                                                             58.48;
                                                                                                                                                                                                                                                                                   12 MAHFILFVFTVSTIFHVQQR--
                                                                                                                                                                                                                               Matches 209; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                 315
                                                                                349
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                                                                                                                               365 AA;
                                                                                                                                                                                                          Similarity
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                                 315
                                                                                349
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                                                                                                                                 SEQUENCE
                                                                                                                                                                                   Query Match
                                 VARIANT
                                                                                   VARIANT
                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232
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333
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                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
LUMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 PVAIFCLAGTPVHFNASDSCPKHPASLSGTWTIYPDGRFGNQMGQYATLLALAQLNGRQA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 FIPAQMHSTLAPIFRITLPVLHSATASRIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 PVQIPVLAST-----SKALGPSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPA 93
                                                                                                       -!- PATHWAY: GLYGOSYJATION.
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
FORM IN TRANS CLOSTERNAE OF GOLGI.
-!- MISCELLANEOUS: THERE ARE TWO GENES (FUTI AND FUT2) WHICH ENCODE
GALACTOSIDE 2-L-FUCOSYLTRANSFERASE. THEY ARE EXPRESSED IN A
TISSUE-SPECIFIC MANNER.
O status and susceptibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWTFYHHLRQEILQEFTLHDHVREEAQKFLRGLQV - NGSRPGTFVGVHVRRGDYVHVMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212 KVWKGVVADRRYLQQALDWFRARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAKDFALLIQCNHTIMTIGTFGIWAAYLIGGDTIYLANYTLPDSPFLKIFKPEAAFLPEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.4%; Score 1079.5; DB 1; Length 365; 65.5%; Pred. No. 3.4e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR00216; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal-anchor; Golgi stack; Polymorphism.
                                                                                                                                                                                                                                           SIMILARITY; BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11
determine erythrocyte antigen precursor O status and suscep
Escherichia coli F18 colonization in the Small intestine.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
*!- CATALIYTIC ACTIVITY: GDP-L-fucose + beta-D-galactcsyl-R
alpha-L-fucosyl-1,2-beta-D-galactcsyl-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66; Indels
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DAFCE77E89A29D75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A -> T.
R -> Q.
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^ ^
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U70883; AAB81884.1; -.
EMBL; AF136896; AAF59833.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41106 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L50534; AAB02984.1; -.
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365
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103
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365 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
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Best Local (
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                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi:
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae: Rattus.
NCBL_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                           (Secretor blood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         273 AKDFALLTQCNHTIMTIGTFGIWAAYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213 VWKGVVADRRYLQQALDWFRARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 98 N-LINKED (GLCNAC. . .) (POTENTIAL)
159 AA; 17250 MW; 14DECEB7C2E6384A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 159;
                                      Galactoside 2.L.fucosyltransferase 2 (EC 2.4.1.69) (Secret group alpha-2-fucosyltransferase) (GDP-L.fucose:beta-D-galactoside 2-alpha-L.fucosyltransferase 2) (Alpha(1,2)FT (Fucosyltransferase 2) (Alpha(1,2)FT (Fucosyltransferase 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                n
Similarity 88.5%; Pred. No. 1.7e-46;
16; Conservative 6; Mismatrher
(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA.
                                                                                                                                                                                                                                                                                                                        MEDLINE=94280382; PubMed=8010942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TXQ7_CAEEL

ID YKQ7_CAEEL STANDARD; F

AC P34302;

DT 01-FEB-1994 (Rel. 28, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L26010; AAB41515.1;
                                                                                                                                                           Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIAADLSPLLK 343
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                                                                                                                                       OR SEC1 OR FIB
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                     15-JUN-2002
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NON_TER
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159 AA.

PRT;

FUT2_RAT STANDARD; F Q10984; 01-0CT-1996 (Rel. 34, Created)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
                                                                                                                         SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=Bristol N2;
WILSON R., Alnscough R., Anderson K., Baynes C., Berks M.,
Wilson R., Alnscough R., Anderson K., Copsey T., Cooper J., Coulson A.,
Carkon M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Johnston L., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Sins M., Smmldon N., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Meg J., Ihomas K., Vaudin M., Vaughan K.,
watesfor R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 ASTARLANHIFELVSVYGMAKSLNRKPAIFVEDSKYNLLITGVRKVLPGLLDEFQIFEYP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 -HSATASRIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHD 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269 EGSPAKDFALL-TQCNHTIMTI--GTFGIWAAYLTGGDTIYLANY-TLPDSPFLK-IFKP 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 NAIGREGNOMGEYATLYALAK-MNGRPA-FIPAQMHSTLAPIFRITLPVL------ 114
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative glycosyl transferase C06El.7 in chromosome III (EC 2.-.-.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LFVFTVSTIFHVQQRLAKIQAMWELPVQIPVLAS------TSKALGPSQLRGMWT--I 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 LLCVLVVVLFFINNQFVQ-RTTWSRGLRSPFLDSRIFQEKSEIERSTLPPIPKGFLSSKL 68
                                                                    Eukaryota, Metazoa; Nematoda, Chromadorea, Rhabditida, Rhabditoidea;
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 VHN-KATKVPLSEKCCIFDNPDKFNNI-SSEYLHLTGH----FY-----QSWKYFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 HVREEAQKFLRGL----QVNGSRPGTFVG---VHVRRGDYV---HVMPKVWKGVVADRRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 KYKEKVOSFVKPAIDFSPLPNSDSSNFISRICIHIRRIDFVDGQHHSSNV----SF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 LQQALDWFRAR----YSSLIFVVTSN-----GMAWCRENIDTSHGDVVFAGDGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 IKPALEFIKEREQKDVNKKMLTVIMGDDPDFEAKMFEGTVRAKKEAKIEETTKYFVS---
                                                                                                                                                                                                                                                                                                                         72.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                              Waterston R.; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 149; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WormPep; C06E1.7; CE30483.
InterPro; IPR002516; GT_11.
Pfam; PF01531; G1yco_transf_11; 1.
Hypothetical protein; Transferase; G1ycosyltransferase.
SEQUENCE 365 AA; 41991 MW; B5FBCA363F31977F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.4%; Score 155;
21.1%; Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L16559; AAA27932.2; -.
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                                                                                                                                                                                                                                                                                                                                                     Nature 368:32-38(1994).
                                                         Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                   NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ry ...
st Local Simi-
                                                                                                                                                                                                                                                                                                             Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                               REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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    QΩ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Uozumi N., Yanagidani S., Miyoshi E., Ihara Y., Sakuma T., Gao C.-X., Teshima T., Fuji S., Shiba T., Taniguchi N.; "Purification and cDNA cloning of porcine brain GDP-L-Fuc:N-acetyl-beta-D-glucosaminide alphal-->6fucosyltransferase."; J. Biol. Chem. 271:27810-27817(1996).

-!- FUNCTION: Catalyzes the addition of fucose in alpha 1-6 linkage to the first Glonac residue, next to the peptide chains in N-glycans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SH3-BINDING (POTENTIAL)
IMPORTANT FOR DONOR SUBSTRATE BINDING (BY
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The pH optimum is 7.

-!- CATALYTIC ACTIVITY: GDP-L-fucose + N4-(N-acetyl-beta-D-glucosaminyl-1,2-alpha-D-mannosyl-1,3-(R(1)-alpha-1,6)-beta-D-mannosyl-beta-N-acetyl-1,4-N-acetyl-D-glucosaminyl-1,4-N-acetyl-D-glucosaminyl-1,2-alpha-D-mannosyl-1,3-(R(1)-alpha-1,6)-beta-D-glucosaminyl-1,2-alpha-D-mannosyl-1,3-(R(1)-alpha-1,6)-beta-D-mannosyl-1,4-n-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               779282;
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Alpha-(1,6)-fucosyltransferase (EC 2.4.1.68) (Glycoprotein 6-alpha-L-fucosyltransferase)
fucosyltransferase) (GDP-fucose--Glycoprotein fucosyltransferase)
(GDP-L-Fucinal Ascetyl beta-D-glucosaminide alphal,6-fucosyltransferase)
283 ENTPQDDLAYSHYSCDATLITAPSSTFGWWLGYLSKGQAVYYQDIRSTNDVNYKKGVLDP 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glucosaminyl)aspáragine.

--- PATHWAY: Glycosylation.

--- SUBCELLULAR LOCATION: Type II membrane protein. Membrane-bound form in trans cisternae of Golgi (By similarity).

--- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN BRAIN.

--- SIMILARITY: COWTAINS 1 SH3 DOMAIN.

--- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transferase; Glycosyltransferase; Transmembrane; Signal-anchor;
Golgi stack; SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., SEQUENCE OF 102-130; 333-344; 402-415 AND 566-575, AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LUMENAL, CATALYTIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   575 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (alphal-6FucI) (Fucosyltransferase 8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97066976; PubMed=8910378;
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Pfam; PF00018; SH3; 1.
SMART; SM00326; SH3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                              EAAFLPEWTGIAAD 337
                                                                                                                                                                                343 DDFFVPSWTSIMLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            566-575, AND
TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
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FUT8_PIG
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Genew;
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OBWC5; QBPXC6; QP2U5; QPP2U6; 000235;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last cannotation update)
Alpha-(1,6)-fucosyltransferase (EC 2.4.1.68) (Glycoprotein 6-alpha-L-fucosyltransferase) (GDP-L-Fuc:N-acetyl-beta-D-glucosaminide alpha1,6-fucosyltransferase)
                                                                                                                                                                                                                384
                                                                                                                                                                                                                                                                      443
                                                                                                                                                            --GEVKDKNVQVVELPIVDSVHPRPPYLPLAVPEDLAD----RLVRVHGDPA--VWWVSQ 330
                                                                                                                                                                                      HL-----NDWMBEE-----YRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLH 172
                                                                                                       225 HHVVYCFMIA--YGTORTLALESHNWRYATGGWETVFRPVSETCTDRSGSS--TGHWS-- 278
                                                                                                                                 AIGRLGNOMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATASRIPWONY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Purification and cDNA cloning of GDP-L-Fuc:N-acetyl-beta-D-glucosaminide:alphal-6 fucosyltransferase (alphal-6 FucT) from human gastric cancer MKN45 cells.";
7. Biochem. 121:626-632(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ς;
                                                                             14 HFILFVFTVSTIFHVQQRLAKIQAMWEL-----PVQIPVLASTSKALGPSQLRGMWTIN 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ж
.;
                                                                                                                                                                                                       DHYREEAQKFLRGLQVNGSR-----PGTFVGVHVRRGDYVHVMPK--VW-----
                                                                                                                                                                                                                                                                      - HVEEDFQLLARRMQVDKKRVYLATDDPALLKEAKTKYPSYEFISDNSISWSAGLHNRYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sasho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A sequence motif involved in the donor substrate binding by alphal, 6-fucosyltransferase: the role of the conserved arginine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DONOR SUBSTRATE BINDING, AND MUTAGENESIS OF ARG-365 AND ARG-366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Calileau A., Balanzino L., Candelier J.J., Oriol R., Mollicone "Differential splice variants of human FUT8 embryonic cDNA."; Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                         ENSLRGVILDIHFLSQA-DFLVCTFSSQV------CRVAYEIMQALHPD 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fanagidani S., Uozumi N., Ihara Y., Miyoshi E., Yamaguchi N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE~20229550; PubMed=10764839;
Takahashi T., Ikeda Y., Tateishi A., Yamaguchi Y., Ishikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yameguchi Y., Ikeda Y., Takahashi T., Ihara H., Tanaka T., Oboumi N., Yanagidani S., Inoue S., Fujii J., Taniguchi N.; "Genomic structure and promoter analysis of the human alphal, 6-fucosyltransferase gene (FOTB).",
                                                                                                                                                                                                                                                                                                 ----KGVVADRRYLQQALDWFRARYSSLIFVVTSNGMAWCR---ENIDTSHGD
                         5.0%; Score 92; DB 1; Length 575; 20.5%; Pred. No. 2.6;
 0F199D0BC2018F7B CRC64;
                                                     108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1), AND FUNCTION. MEDLINE=97279058; PubMed=9133635;
                                                     47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (alphal-6FucT) (Fucosyltransferase 8). FUT8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20275614; PubMed=10814706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1).
 66229 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ycobiology 10:637-643(2000)
                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
  575 AA;
                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Embryo;
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                                                       60;
    SEQUENCE
                            Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseé1sb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMPORTANT FOR DONOR SUBSTRATE BINDING.
EVKDKNVQVVQLPIVDSLHPRPPYLPLAVPEDLADRLVRVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDPAVWWVS -> TPIMNLLVITLFPGQLDCTIDTQKIHFV
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225 HHVVYCFMIAYGTQRTLILESQNWRYATGGWE-TVFRPVSETCTDRSGIS--TGHWS--- 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 HFILFVFTVS-----TIFHVQQRLAKIQAMWELPVQIPVLASTSKALGPSQLRGMWIINA 68
                                                                                                                                                                                                                                                        -i- PATHWAY: Glycosilation.
-i- SUBCELIDIAR LOCATION: Type II membrane protein. Membrane-bound form in trans cisternee of Golgi (By similarity).
-i- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2/retinal; are produced by alternative splicing.
-i- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-i- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MISSING (IN ISOFORM 2).
R->A, K: COMPLETE LOSS OF ACTIVITY.
R->A, K: DECREASES ACTIVITY TO 3%.
5AE24A93881E18D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       !ransferase; Glycosyltransferase; Transmembrane; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LUMENAL, CATALYTIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.9%; Score 90; DB 1; Length 575; 20.2%; Pred. No. 3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SH3 domain, Alternative splicing.

1 9 CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SH3-BINDING (POTENTIAL)
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EMBL, AB049740; BAB40929.2; --
EMBL, AB032573; BAA92885.2; --
EMBL, AB032572; BAA92888.1; --
EMBL, AB032568; BAA92888.1; JOINED.
EMBL, AB032569; BAA92888.1; JOINED.
EMBL, AB032569; BAA92888.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AF038281; AAB92372.2; --
EMBL, AF038280; AAB92372.2; JOINED.
EMBL; X17979; CAA76988.1; --
EMBL; X17976; CAA76986.1; --
EMBL; X17977; CAA76986.1; --
EMBL; X17978; CAA76986.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAA92858.1; JOINED
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                                                                                                                                                                                                                                      glucosaminyl)asparagine.
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Pfam; PF00018; SH3; 1.
SMART; SM00326; SH3; 1.
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366
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575 AA;
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MUTAGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformatics and the EMBL outstation—
the European Bioinformatics Institute. There are no restrictions on its
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modified and this statement is not removed. Usage by and for commercial
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or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: GDP-L-fucose + N4-(N-acetyl-beta-D-glucosaminyl-1,2-alpha-D-mannosyl-1,3-(R(1)-alpha-1,6)-beta-D-mannosyl-beta-N-acetyl-1,4-D-glucosaminyl-1,4-N-acetyl-D-glucosaminyl-1,4-N-acetyl-D-glucosaminyl-1,2-alpha-D-mannosyl-1,3-(R(1)-alpha-1,6)-beta-D-mannosyl-1,4-beta-D-mannosyl-1,4-beta-D-mannosyl-1,4-beta-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-glucosaminyl-1,4-(alpha-L-fucosyl-1,6)-N-acetyl-D-
                                                                                                                                                                                                                                                                                                                                                                               O9WTS2; Q92IU1;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (GP) (GDP-Incose-Julycoprotein fucosyltransferase)
(GDP-Incosyltransferase) (GDP-Incose-Julycoprotein fucosyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. Submitted (JUL-2001) to the addition of fucose in alpha 1-6 linkage to the first Glonac residue, next to the peptide chains in N-glycans
69 IGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATASRIPWQNYH 128
                       385 HVEEHFOLLARRMQVDKKRVYLATDDPSLLKEAKTKYPNYEFISDNSISWSAGLHNRYTE 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glucosaminyl)asparagine.
PATHWAY: Glycosylation.
SUBCELLULAR LOCATION: Type II membrane protein. Membrane-bound form in trans cisternae of Golgi (By similarity).
SIMILARITY: CONTAINS I SH3 DOWAIN.
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSPERASE FAMILY 23.
                                                                           ----YRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHD
                                                                                                                                                   174 HVREEAQKFLRGLQVNGSR-----PGTFVGVHVRRGDYVHVMPK--VW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                             332 VKYLIRPQPWLEKEIEEATKKLGFKHPVIGVHVRRTDKVGTEAAFHPIEEYMV-----
                                                                                                                                                                                                                                                                445 NSLRGVILDIHFLSQA-DFLVCTFSSQV------CRVAYEIMQTLHPD 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashi H., Yoneda A., Asada M., Ikekita M., Imamura T.; "Molecular cloning of mouse alpha-1,6-fucosyltransferase and expression of its mRNA in the developing cerebrum."; DNA Seq. 11:91-96(2000).
                                                                                                                                                                                                                            ---KGVVADRRYLQQALDWFRARYSSLIFVVTSNGMAWCR---ENIDTSHGD
                                                                                                                                                                                                                                                                                                                                                             575 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (alphal-6FucT) (Fucosyltransferase 8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IISSUE=Brain;
MEDLINE=20358720; PubMed=10902914;
                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                           129 L----NDWMEEE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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FUT8_MOUSE
ID FUT8_MOUSE
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EMBL; AB025198; BAA76392.1; -. EMBL; BC010666; AAH10666.1; -.

InterPro; IPR001452; SH3

MGD; MGI:1858901; Fut8

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 IGRLGNOMGEYATLYALAKMNGRPAFIPAOMHSTLAP-IFRITLPVLHSATASRIPWONY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   279 -GEVNDKNIQVVELPIVDSLHPRPPYLPLAVPEDLADRLLRV-----HGDPA--VWWVSQ 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HL----NDWMEEE----YRHIPPGEYVRFTGYPCSWTFYHHLROEILOEFTLH 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -HVEQHFQLLARRMQVDKKRVYLATDDPTLLKEANTKYSNYEFISDNSISWSAGLHNRYT 443
                                                                                     CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                        14 HFILEVFTVS-----TIFHVQQRLAKIQAMWELPVQIPVLASTSKALGPSQLRGMWTINA 68
                                                                                                                                                              SH3.
SH3-BINDING (POTENTIAL).
SH3-BINDING (POTENTIAL).
T -> S (IN REF. 2).
C -> E (IN REF. 2).
C -> E (IN REF. 2).
T -> K (IN REF. 2).
T -> K (IN REF. 2).
T -> K (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          331 FVKYLIRPQPWLEKEIEEATKKLGFKHPVIGVHVRRTDKVGTEAAFHPIEEYMV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 DHYREEAQKFLRGLQVNGSR-----PGTFVGVHVRRGDYVHVMPK--VW-----
                            PROSITE: PS50002; SH3; FALSE NEG.
Transferase; Glycosyltransferase; Transmembrane; Signal-anchor; Golgi stack; SH3 domain.
                                                                                                                                                                                                                                                                                                                                                    78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----KGVVADRRYLQQALDWFRARYSSLIFVVTSNGMAWCR---ENIDTSHGD 260
                                                                                                                             (POTENTIAL).
LUMENAL, CATALYTIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 575;
                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                               DB 1;
3.8;
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                                                                                                                                                                                                                                                                                                                 4.9%; Score 90;
                                                                                                                                                                                                                                                                                                                                    Pred. No.
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                                                                                                                                                                                                                                                                              66555 MW;
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es 58; Conservative
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305
366
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388
Pfam; PF00018; SH3; 1.
SMARI; SM00326; SH3; 1.
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502
2999
365
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418
575 AA;
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                                                                       Golgi stack;
DOMAIN
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CONFLICT
SEQUENCE
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Job time
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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using sw model protein search, OM protein

May 27, 2003, 15:01:52; Search time 36.6774 Seconds Run on:

(without alignments) 1932.533 Million cell updates/sec

US-10-040-863-11 1850 Title: Perfect score:

1 MLVVQMPFSFPMAHFILFVF......AAFLPEWTGIAADLSPLLKH 344 Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

671580 segs, 206047115 residues

Searched:

Total number of hits satisfying chosen parameters:

length: 0 Length: 2000000000 Minimum DB seq Maximum DB seq Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SPTREMBL 21:* Database

sp_invertebrate:*
sp_manmal:*
sp_mhc:*
sp_organelle:*
sp_phage:*
sp_phage:*
sp_plant:*
sp_rodent:* sp_vertebrate:*
sp_unclassified:* sp_rvirus:* sp_bacteriap:* sp_archeap:* sp_archea:* sp_bacteria:* sp_virus:* sp_fungi:* sp_human:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Ogtuda gorilla gor 077486 gorilla gor 077485 pan troglod 09tud5 pan troglod 09ttc7 hylobates 1 099450 homo sapien 077487 pongo pygma 077712 cercopithec 01438 homo sapien 029509 oryctolagus 035087 rattus norv Description SUMMARIES Q29505 035087 077486 077485 09TUD5 09TTC7 099450 077487 DB Query Match Length Score 1825.5 1821.5 1815.5 1793.5 1771.5 1771.5 1736.5 1736.5 1736.5 1736.1 1821.5 1483 No. Result

mus musculu rattus norv

mus musculu rattus norv

Q9JK44 O70504

1475.5 1471.5

O9TSL5

Q9R275

Q9ts15 macaca fasc

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ALIGNMENTS

6. ROMWINAIGRIGNOMGEYATLYALAKMNGRPAFIDAQMHSTLAPIFRITLPVIHSATAS 120 Gaps 1 MLVVQMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAMWELPVQIPVLASTSKALGPSQL 60 "Evolution of alpha2-Fucosyltransferase genes in primates: relation between an intronic Alu-Y element and red cell expression of ABH antigens."

MAOL Biol. Evol. 17:337-351(2600).

EMBL, AF080606; AAF14068.1; -...
InterPro; IPR00216; CT_11.

Pfam: PF01531; Glyco_transf_11; 1. Gorilla gorilla (gorilla). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilia. NCBI_TaxID=9593; 1; Length 343; Apoil P.-A., Roubinet F., Despiau S., Mollicone R., Oriol R., Blancher A.; Indels 343 AA; 39001 MW; A753375D47AE8C8C CRC64; 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Alpha (1,2) fucosyl transferase DB 6; 98.7%; Score 1825.5; DB 6 99.4%; Pred. No. 6.7e-162; 0; Mismatches PRT; MEDLINE=20188794; PubMed=10723735; Best Local Similarity 99.4 Matches 342; Conservative PRELIMINARY; [1] SEQUENCE FROM N.A. STRAIN-ALEXIS SEQUENCE Query Match Q9TUD3 RESULT 1 Q9TUD3 ŏ qq ŏ

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Q9TUD5 PRELIMINARY; PRT; Q9TUD5; 01-MAX-2000 (TYEMBLrel. 13, Created)
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                                                                                                                                                                                         PRT;
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98.8%;
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Primates;
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01-NOV-1998 (TrEMBLrel.
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Mammalia; Eutheria;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                             NCBL_TaxID=9598;
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Koda Y., Tachida H., Soejima M., Takenaka O., Kimura H.;

Koda Y., Tachida H., Soejima M., Takenaka O., Kimura H.;

"The old origin of a null allele se428 of the human ABO-secretor type alpha(1,2) fucosyltransferase gene (FUT2).";

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 KFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIF 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVISNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RGMWTINAIGRLGNOMGEYATLYALAKMNGRPAFIPAOMHSTLAPIFRITLPVLHSATAS 120
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                                          RIPWONYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHDHVREEAQ 180
RGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATAS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MLVVQMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAMWELPVQIPVLASTSKALGPSQL
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                                                                                                                                                     VVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Gorilla.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycosyltransferase, Transferase.
SEQUENCE 343 AA, 38973 MW; 894E28BD74AEBFBC CRC64;
                                                                                                                                                                                                                                                                                                                                   GGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 344
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20, Last annotation update)
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Mammalia; Eutheria; Primates;
NCBI_TaxID=9593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alpha(1,2) fucosyltransferase.
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SEQUENCE FROM N.A.

MEDLINE-95181460; PubMed=7876235;

Kelly R.J., Rouguler S., Giorgi D., Lennon G.G., Lowe J.B.;

Kelly R.J., Rouguler S., Giorgi D., Lennon G.G., Lowe J.B.;

Sequence and expression of a candidate for the human secretor blood group alpha(1,2) fucosyltansferase gene (FUT2).";

J. Biol. Chem. 270:4640-4649(1995).

EMBL; AB015634; BA33127.1;

Interpro; IPR002516; GT_11.

Ffan, PF01531; G1yco_transf_11; 1.

Ffan, PF01531; G1yco_transf_11; 1.

Glycosyltransferase; Transferase.

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Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                     301 GGDTIXLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 344
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Pred. No. 5.8e-161;
1; Mismatches 2;
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between an intronic Alu-Y element and red cell expression of
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fucosyltransferase.
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"Evolution of alpha2-Fucosyltransferase genes in primates: relation
                                                                                                                                                                       "Evolution of alpha2-Fucosyltransferase genes in primates: relation between an intronic Alu-Y element and red cell expression of ABH
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Mammalia, Butheria, Primates, Catarrhini, Hylobatidae, Hylobates.
                                                                   Euteleostomi;
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Appil P.-A., Roubinet F., Desplau S., Mollicone R., Oriol
Blancher A.;
                                                                                                                                                                                                                                                                                           96.9%; Score 1793.5; DB 6; Length
98.8%; Pred. No. 6.4e-159;
Live 1; Mismatches 2; Indels
                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butel.
Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Pan.
NCBL_TaxID=9598;
                                                                                                                                                                                                                                                                      338 AA; 38428 MW; E7FABAOFF1BC95F9 CRC64;
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01-MAY-2000 (TYEMBLIE). 13, Last sequence update)
01-MAR-2002 (TYEMBLIE). 20, Last annotation update)
Alpha(1,2)fucosyltransferase.
        01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Alpha (1,2) fucosyl transferase.
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                                                                                                                                                                                                   antigens.";
Mol. Biol. Evol. 17:337-351(2000).
EMBL, APD80604; AAF14066.1; -.
Interpro; IPR002516; GT_11.
Pfam: PF01531; Glyco_transf_11: 1.
Transferase.
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                                                         Pan troglodytes (Chimpanzee)
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J. Blol. Chem. 271:9830-9877(1996).
EMBL; D89326: BAA13943.1;
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Kudo T., Iwasaki H., Shinya N., Nishihara S., Ando T., Narimatsu I.,
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Bukaryota; Metazoa: Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                            96.5%; Score 1784.5; DB 6; Length 343; 97.4%; Pred. No. 4.5e-158; Live 2; Mismatches 6; Indels 1;
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                                                                                                                                   A52161BE67E1F64D CRC64;
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03, Last sequence update)
20, Last annotation update)
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antigens.";
Mol. Biol. Evol. 17:337-351(2000).
BMBL, AB136648: AAF25585.1;
Interpro; IPR002516; GT_11.
Pfan; PP01531; Glyco_Lransf_11; 1.
Glycosyltransferase; Transferase.
SEQUENCE 343 AA; 39059 MW; A5216
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LGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHSATASRIPWQNYHLND 131
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                                                                                                                    180 RPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYSSLIFVVTSNGMAWCR
                                                                                                                                            ENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLTGGDTIYLANYT
                                                WMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHDHVREEAQKFLRGLQVNGS
                                                                                                                                                                                                                                                                                                                                                            Pongo pygmaeus (Orangutan).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
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"Sequence and expression of a candidate for the human secretor group alpha(1, 2) fucosyltansferase gene (FUT2).";
J. Biol. Chem. 270:4449(1995).
BMBL; AB015636; BAA31129.1;
InterPro: IPR002516; GT_11.
Pfam; PF01531; Glyco_transferase.
SEQUENCE 343 AA, 38973 MW; 2BD4D2A9704E4A0C CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 20, Last annotation update)
Alpha(1,2) fucosyltransferase.
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                                                                                                                                                                                                                                                                             343 AA
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
MEDLINE-99181460; PubMed=7876235;
KRELINE-99181460; PubMed=7876235;
KRELIN Rouguler S., Glorgi D., Lennon G.G., Lowe J.B.;
"Sequence and expression of a candidate for the human secretor blood group alpha(1,2) fuccosyltansferase gene (FUT2).";
Biol. Chem. 270:4640-449(1995).

EMBL; D87934; BAA31692.1;
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241 VVTSNGMAWCRENIDISHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWAAYLT
                                   1 MINIOMPESESMAHFILEVETVSTIFHIQQRLAKFQAMWELSVQIPGLASTSEALQPSQL
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Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
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(TrEMBLrel. 08, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
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Pfam; PF01531; Glyco_transf_11; 1.
Glycosyltransferase; Transferase.
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NCBL_TaxID=37765;
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(TrEMBLrel. 20, Last annotation update)
2-L-fucosyltransferase 3 (EC 2.4.1.69) (Secretor blood
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"Molecular basis for secretor type alpha(1.2)-fucosyltransferase deficiency in a Japanese population: a fusion gene generated by unequal crossover responsible for the enzyme deficiency.";
Am. J. Hum. Genet. 59:343-350(1996).
                                                                                                                         Eukaryota; Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
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                                                             Last sequence update)
Last annotation update)
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             346
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|-FEB-1997 (TrEMBLrel, 02, Last sequ
|-MAR-2002 (TrEMBLrel, 20, Last anno
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Pfam: PF01531; Glyco_transf_11; 1.
Glycosyltransferase; Transferase; SEQUENCE 346 AA; 39395 MW; 9D72
               PRT;
                                                                                                                                                                                                                                                         SECUENCE OF 84-106 FROM N.A.
MEDLINE=96335703; PubMed=8755920;
                                                                                              Alpha (1, 2) fucosyltransferase.
Homo sapiens (Human).
                                              01-NOV-1996 (TrEMBLrel. 01,
01-JAN-1998 (TrEMBLrel. 05,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                            PARTIAL SEQUENCE FROM N.A.
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Best Local Similarity
Matches 295; Conserve
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                                                                                                                                                                NCBI_TaxID=9606;
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01-MAR-2002 (
Galactoside 2
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               Q14338
Q14338;
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TISSUE-SEXPROINTESTUNAL TRACT;

REQUENCE FROM N.A.

IISSUE-GASTROINTESTUNAL TRACT;

AM HILDSH'S., KOJIMA N., KANAZAWA I., TSUJI S.;

HILDSH'S., KOJIMA N., KANAZAWA I., TSUJI S.;

AM HEDLINE-96279281; PubMed-8663188;

TWO-CALPH C.COADIMA N., KANAZAWA I., TSUJI S.;

TUCOSG:DETA-D-GAJALOSTOSIGE 2-alpha-L-fucosyiLtransferase.";

L. BIOL, Chem. 271:16975-16981 (1996).

THE HANTICEN PREATES A MEMBRANE-ASSOCIATED PRECURSOR OLIGOSACCHARIDE

TOWALTION: CREATES POR THE FINAL STEP IN THE MEMBRANE-ASSOCIATED

TOWAL AND B ANTICEN SYNTHESIS PATHWAY. H AND SE BUXYMES PUCOSYLATE THE

SAME ACCEPTOR SUBSTRATES BUT EXHIBIT DIFFERENT KW VALUES.

AND BARTACT GAPLAYINIY. GBP-L-FUCOSE + BETA-D-GALACIOSYL-R = GDP +

ALPHA-L-FUCOSYL-1.2-BETA-D-GALACIOSYL-R = GDP +

ALPHA-L-FUCOSYL-1.1.2-BETA-D-GALACIOSYL-R = GDP +

ALPHA-L-FUCOSYL-1.1.2-BETA-D-GALACIOSYL-R = GDP +

ALPHA-L-FUCOSYL-1.1.2-BETA-D-GALACIOSYL-R = GDP +

ALPHA-L-FUCOSYL-1.1.2-BETA-D-GALACIOSYL-R = GDP +

AND RESELUCIAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND

FORM IN TRANS CISTERNED OF GOLG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SRPLGGMWTINAMGRLGNQMGEYATLYALAKENGRPAYIPAQMHSTLAPIFRISLPVLHS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MLVVQMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAMWE--LFVQIPVLA--STSKALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 PSQLRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 ATASRIPWONYHLNDWMEEBYRHIPPGBYVRFTGYPCSWTFYHHLRQEILQEFILHDHVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 EEAQKFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EBAQAFLRGLRVNGSRPSTFVGVHVRRGDYVRVMPQVWKGVVADRGYLEQALDWFRARYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- TISSUE SPECIFICITY: ADULT GASTROINTESTINAL TRACT AND COLON.
-!- MISCELLANBOUS: THERE ARE IRREE GENES (FUT1, FUT2 AND FUT3) WHI
BUCODE GALACTOSIDE 2-L-FUCOSYLTRANSFERASE IN RABBIT. THEY ARE
EXPRESSED IN A TISSUE-SPECIFIC MANNER.
-!- SIMILARITY: STRUCTURAL SIMILARITY WITH THE OTHER MAMMALIAN
                                                            Euteleostomi;
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N-LINKED (GLCNAC. ) (POIENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

746F7007309862A5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01531: Glyco_transf=11; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
Signal-anchor; Golgi stack.
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Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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39469 MW;
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347 AA;
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                                                                                                    NCBI_TaxID=9986;
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DOMAIN
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Best Local
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Matches 276;
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Q9JL27;
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                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                        1 MLVVQMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAM--WELPV------QIPVLA 49
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
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                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                         DB 11; Length 354;
                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                              fucosyltransferase genes.";
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB006138; BAA21742.1;
                                                                                                                                                                                                                                                                      InterPro: IPR002516; GT_11.
Pfam; PF01531; Glyco_transf_11; 1.
Glycosyltransferase; Transferase.
SEQUENCE 354 AA; 39995 MW; 86364448B8215BA1 CRC64;
                                                                                                                                                                                                         Soejima M., Wang B., Koda Y., Kimura H.; "Two distinct rat GDP-L-fucose:b-D-galactoside 2-a-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last annotation update)
                                               (TrEMBLrel. 05, Created)
(TrEMBLrel. 05, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                 37;
                                                                                                                                                                                                                                                                                                                                      80.2%; Score 1483; DB 11; 77.7%; Pred. No. 6.1e-130; iive 30; Mismatches 37;
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
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                           PRT;
                                                                                       Alpha 1,2-fucosyltransferase.
FTB.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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FTB.
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                           PRELIMINARY;
                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=COLON CANCER;
                                                                                                                                                                                                                                                                                                                                                      Similarity
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01-JAN-1998
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"Molecular Cloning, Genomic Mapping, and Expression of Two Secretor Blood Group alpha (1,2)Fucosyltransferase Genes Differentially J. Biol. Chem. 276:23748-23756(2001).

Biol. Chem. 276:23748-23756(2001).

EMBL. AF214656; AR45146:1;
EMBL. MGD; MGD; MGD; MCD; MGCD; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 MFRARYSSPYFVVTSNGMAWCRENINASRGDVVFAGNGIEGSPAKDFALLTQCNFTIMTI
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
Liehr T., Le Pendu J.;
"Comparison of the three rat GDP-L-fucose: beta-D-galactoside
alpha-L-fucosyltransferases FTA, FTB and FTC.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 GTFGIWAAYLAGGDTIYLANYTLPDSPFLKVFKPEAAFLPEWVGIPADLSPLLKH
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                                                                                                                                                 EMBL: J. Blochem. 268 1006-1019(2001).

EMBL: AF131238; AAD24469.1; -
InterPro; IPR002516; GT_11.

Pfam. PF01531; Glyco_transf_11; 1.

Glycosyltransferase.

SEQUENCE 354 AA, 39983 MW; 123E8C8379E8559E CRC64;
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1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Alpha(1,2)fucosyltransferase FUT2 (EC 2.4.1.69).
FUT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1481; DB 11;
Pred. No. 9.4e-130;
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Glycosyltransferase; Transferase.
SEQUENCE 347 AA; 39243 MW; DD5E
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MEDLINE=21316545; PubMed=11323419;
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77.78;
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Best Local Similarity 79.3'
Matches 276; Conservative
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Best Local Similarity
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Lin B., Hay
Iwamori M.;
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"An amino acid region at the N-terminus of rat hepatoma H35 cell GDP-fucose:GM1 alpha 1-2 fucosyltransferase is required for optimum enzyme activity and interaction with lipids.";

Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF264005; AAF72200.1;

InterPro: IPR002116; GT_11.

Pfam; PF01531; Glyco_transf-11; 1.

Glycosyltransferase; Transferase.

SEQUENCE 380 AA; 42742 MW; 920692C96689C05C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 TLHDHVREEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPNVWKGVVADRGYLEKALD 239
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                                                                                                            EEAQKFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALDWFRARYS 236
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                                                                                                                                                                                                          SLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTIGTFGIWA 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MLVVQMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAM--WELPV------QIPVLA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 TLPVLHSATASRIPWQNYHLNDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170 TLHDHVREEAQKFLRGLQVNGSRPGTFVGVHVRRGDYVHVMPKVWKGVVADRRYLQQALD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WFRARYSSLIFVVTSNGMAWCRENIDTSHGDVVFAGDGIEGSPAKDFALLTQCNHTIMTI
240 SPVFVVTSNGMAWCRENINISLGDVVFAGNGIEGSPAKDFALLIQCNHIIMTIGTFGIWA
                                                                                             ATASRIPWQNYHINDWMEEEYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQEFTLHDHVR
                                        60 ---LRGMWTINAIGRLGNQMGEYATLYALAKMNGRPAFIPAQMHSTLAPIFRITLPVLHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.7%; Score 1475; DB 11; Length 380; 77.7%; Pred. No. 3.8e-129; Live 30; Mismatches 37; Indels 12
                                                                                                                                                                                                                                                                               300 AYLAGGDIYLANYTLPDSPFLKIFKPAAAFLPEWMGIPADLSPLLKH 347
                                                                                                                                                                                                                                                                 297 AYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 344
                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                380 AA
                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Alpha 1-2 fucosyltransferase.
Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             275;
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ATASRIPWONYHLNDWMEBBYRHIPPGEYVRFTGYPCSWTFYHHLRQEILQBFTLHDHVR 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 EEAQAFLRGLRVNGSQPSTFVGVHVRRGDYVHVMPKVWKGVVADRGYLEKALDRFRARYS 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MLVVQMPFSFPMAHFILFVFTVSTIFHVQQRLAKIQAMWELPVQIPVLASTSKALGPSQ-
                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 347;
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                                                                                                                                                                                                                                                        01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
GDP-L-fucose:beta-D-galactoside 2-alpha-1-fucosyltransferase
290 GTFGIWAAYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLK
                             STRIN-ICR; TISSUE-CASTROINTESTINAL TRACT;
MEDLINE-20471982; PubMed-11018479;
Lin B., Hayashi Y., Saito M., Sakakibara Y., Yanagisawa M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297 AYLTGGDTIYLANYTLPDSPFLKIFKPEAAFLPEWTGIAADLSPLLKH 344
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Pfan: PF01531; G1yo__transf_11; 1.
G1ycosylltransferases: Transferase.
SEQUENCE 347 AA; 39215 MM; 616CCB11581C4179 CRC64;
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از ایم ایسان
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79.0%; Pred. No. 7e-129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cycloheximide.";
Biochim. Biophys. Acta 1487:275-285(2000).
EMBL; AF064792; AAC16887.1; ".
                                                                                                                                                                                                                                   Created)
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                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                     (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:109374; Fut2.
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Matches 275; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                     01-AUG-1998
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